



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 125396

TO: Fozia Hamud
Location: 4d64 / 4c70
Thursday, June 24, 2004
Art Unit: 1647
Phone: 272-0884
Serial Number: 10 / 015393

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504
jan.delaval@uspto.gov

Search Notes

125396

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Wednesday, June 23, 2004 8:23 AM
To: Hamud, Fozia; STIC-Biotech/ChemLib
Subject: RE: rush search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 & 1642
(571)-272-0841
Remsen, 3E89

-----Original Message-----


From: Hamud, Fozia
Sent: Wednesday, June 23, 2004 7:56 AM
To: Chan, Christina
Subject: rush search

Hi Christina, 10/015,393 is a date case that I must finish this bi-week. Would you kindly approve this rush search.
Thank you very much.

Stic,

Please search SEQ ID NOs:115 and 116 of 10/015,393 against commercial and interference data bases.

Fozia Hamud
Patent Examiner
Art Unit 1647
Remsen: Room 4D64
Mail box: Remsen 4C70
272-0884

Searcher: 
Phone: 22504
Location: _____
Date Picked Up: 6/23
Date Completed: 6/24
Searcher Prep/Review: _____
Clerical: 20
Online time: 20

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ✓
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 23, 2004, 11:04:51 ; Search time 735 Seconds
(without alignments)
10449.989 Million cell updates/sec

Title: US-10-015-393A-115
Perfect score: 1808
Sequence: 1 gagctaccagcgctggtt.....actctcaactgtgctcattt 1808

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N Geneseq 29Jan04:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1980s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002s:*
 - 7: Geneseqn2003as:*
 - 8: Geneseqn2003bs:*
 - 9: Geneseqn2003cs:*
 - 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1808	100.0	1808	3 AAA37054	Aaa37054 Human PRO
2	1808	100.0	1808	4 AAF54284	Aaf54284 DNA encod
3	1808	100.0	1808	8 ACD68321	Acd68321 Novel hum
4	1808	100.0	1808	8 ACH04423	Ach04423 Human cdn
5	1808	100.0	1808	8 ACD67967	Acd67967 Novel hum
6	1808	100.0	1808	9 ADC17984	Adc17984 Human PRO
7	1808	100.0	1808	9 ADD70630	Add70630 Human cdn
8	1808	100.0	1808	9 ADD33707	Add33707 Human cdn
9	1808	100.0	1808	9 ADD70153	Add70153 Human cdn
10	1808	100.0	1808	9 ADD38274	Add38274 Human cdn
11	1808	100.0	1808	9 ADD33230	Add33230 Human cdn
12	1808	100.0	1808	9 ADD33753	Add33753 Human cdn
13	1808	100.0	1808	9 ADD40184	Add40184 Human cdn
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16	1808	100.0	1808	9 ADE49928	Ade49928 Human cdn
17	1808	100.0	1808	9 ADE21486	Ade21486 Human cdn
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19	1792	99.1	1878	5 AAF93783	Aaf93783 Human cdn
20	1231.4	68.1	1282	4 AAD03940	Aad03940 Human dru
21	1189.8	65.8	1699	4 AAH25133	Aah25133 Nucleotid
22	1189.8	65.8	1699	6 ABK15714	Abk15714 Human 216
23	1150.2	63.6	1195	6 ABK35374	Abk35374 Human cdn

C	24	1098.6	60.8	1335	5	AAD07737	Aad07737 Human sec
	25	1037.4	57.4	1167	4	AAI59543	Aai59543 Human pol
	26	966.4	53.5	2593	4	AAK71133	Aak71133 Human imm
	27	963.2	53.3	2590	4	AAK71135	Aak71135 Human imm
C	28	935.8	51.8	1668	4	AAI61329	Aai61329 Human pol
	29	916.8	50.7	1153	4	AAH25132	Aah25132 Nucleotid
	30	916.8	50.7	1153	6	ABK15713	Abk15713 Human 337
	31	824.4	45.6	4787	3	AAI6282	Aai6282 Human pro
	32	739.2	40.9	847	3	AAI6282	Aai6282 Human sec
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	34	737.6	40.8	847	5	AAD07712	Aad07712 Human sec
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	45	271.6	15.0	904	4	ABL04019	Ab104019 Drosophil

ALIGNMENTS

RESULT 1
ID AAA37054 standard; cdna; 1808 BP.
AC AAA37054;
XX
DT 08-AUG-2000 (first entry)
DE Human PRO1430 (UNQ736) cdna sequence SEQ ID NO:115.

XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX Homo sapiens.
XX WO200012708-A2.
XX 09-MAR-2000.
XX 01-SEP-1999; 99WO-USQ20111.
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 09-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
XX 03-SEP-1998; 98US-0099598P.
XX 09-SEP-1998; 98US-0099602P.
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XX 10-SEP-1998; 98US-0099816P.
XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.

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PR 18-SEP-1998; 98US-0100948P.
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PR 30-SEP-1998; 98US-0102570P.
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PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
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PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
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PR 21-OCT-1998; 98US-0105104P.
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PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
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PR 27-OCT-1998; 98US-0105807P.
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PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
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PR 28-OCT-1998; 98US-0106033P.
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PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106394P.
PR 30-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.

PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106913P.
PR 03-NOV-1998; 98US-0106932P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108805P.
PR 17-NOV-1998; 98US-0108807P.
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PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
PA (GETH ) GENENTECH INC.
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PI WPI: 2000-237871/20.
XX P-PSDB; AAY99372.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small
XX molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Claim 2; Fig 65; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY9340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
XX Sequence 1808 BP; 349 A; 545 C; 571 G; 343 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1808; DB 3; Length 1808;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGCGCGCTGGTGTGAGCAAGCTCCGCGCCGACTCCGAGCGCTGAGCGCT 60
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QY 121 GTAGCAGCGCGCGCTGCTCTCAAGAGCTATGTCTACCGTGGGCTTCCCCAGCAAG 180
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QY 241 ACCGCTTGGAACTGGCCAGGAGGAGGCAACATCATCTGCGCTGCCAGACATGGAG 300
Db 241 ACCGCTTGGAACTGGCCAGGAGGAGGCAACATCATCTGCGCTGCCAGACATGGAG 300
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PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.

XX Claim 2; Fig 65; 787pp; English.

XX The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy

XX Sequence 1808 BP; 349 A; 545 C; 571 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 1808; DB 4; Length 1808;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGGCGGCTGTGTGACGAAGCTCCCGCGGACTCCGGACGGCTGACGGCT 60
DB 1 GAGCTACCCAGGCGGCTGTGTGACGAAGCTCCCGCGGACTCCGGACGGCTGACGGCT 60
QY 61 GAGGCTGTCCCGGCGCGGATGAGCCGCTACCTGCTGCGCTGCGCGCTGGGACG 120
DB 61 GAGGCTGTCCCGGCGCGGATGAGCCGCTACCTGCTGCGCTGCGCGCTGGGACG 120
QY 121 GTAGCAGGCGCGCGCTGTGTGCTCAAGGACTATGTACCGGTGGGCTTGCCCCAGCAAG 180
DB 121 GTAGCAGGCGCGCGCTGTGTGCTCAAGGACTATGTACCGGTGGGCTTGCCCCAGCAAG 180
QY 181 GGCACCATCTGGGAGAGCGTCACTGTCAGCGGCGCCACACAGGCTCGGAGCAG 240
DB 181 GGCACCATCTGGGAGAGCGTCACTGTCAGCGGCGCCACACAGGCTCGGAGCAG 240
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RESULT 3

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RESULT 4						
ACH04423						
ID	ACH04423 standard; cDNA; 1808 BP.					
XX						
AC	ACH04423;					
XX						
DT	01-OCT-2003 (first entry)					
XX						
DE	Human cDNA encoding secreted/transmembrane protein PRO1430.					
XX						
KW	Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnary;					
KW	cardiac; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;					
KW	adrenal cortical capillary; endothelial cell growth; wound healing;					
KW	stimulated T-lymphocyte proliferation; immune response suppression;					
KW	neonatal heart hypertrophy; cardiac insufficiency disorder;					
KW	vascular endothelial growth factor; inflammation; mononuclear cell;					
KW	eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;					
KW	chondrocyte redifferentiation; bone disorder; cartilage disorder;					
KW	sports injury; arthritis.					
OS	Homo sapiens.					
XX						
PN	US2003044841-A1.					
XX						
PD	06-MAR-2003.					
XX						
XX	06-DEC-2001; 2001US-00006856.					
PR	01-SEP-1998; 98US-0098716P.					
PR	01-SEP-1998; 98US-0098723P.					
PR	01-SEP-1998; 98US-0098749P.					
PR	01-SEP-1998; 98US-0098750P.					
PR	02-SEP-1998; 98US-0098803P.					
PR	02-SEP-1998; 98US-0098821P.					

PR	20-OCT-1998;	98US-0105002P.	PR	28-FEB-2001;	2001WO-US006520.	XX	(GETH) GENENTECH INC.
PR	21-OCT-1998;	98US-0105104P.	PR	01-MAR-2001;	2001WO-US006666.	XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Fertara N, Fong S;
PR	22-OCT-1998;	98US-0105159P.	PR	01-JUN-2001;	2001WO-US017800.	PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PR	22-OCT-1998;	98US-0105286P.	PR	20-JUN-2001;	2001WO-US019692.	PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PR	26-OCT-1998;	98US-0105693P.	PR	29-JUN-2001;	2001WO-US021066.	PI	Williams PW, Wood WI;
PR	26-OCT-1998;	98US-0105694P.	PR	09-JUL-2001;	2001WO-US021735.	XX	WPI; 2003-492259/46.
PR	27-OCT-1998;	98US-0105807P.	PR	04-SEP-2001;	2001US-00946374.	DR	P-PSDB; ABO44467.
PR	27-OCT-1998;	98US-0105881P.	XX			XX	Novel secreted and transmembrane polypeptides and polynucleotides
PR	27-OCT-1998;	98US-0106062P.	XX			PT	encoding them useful for treating various cardiac insufficiency
PR	28-OCT-1998;	98US-0106023P.	XX			PT	disorders, bone and/or cartilage disorders such as sports injuries and
PR	28-OCT-1998;	98US-0106030P.	XX			PT	arthritis.
PR	28-OCT-1998;	98US-0106032P.	DR				
PR	28-OCT-1998;	98US-0106178P.	DR				
PR	29-OCT-1998;	98US-0106248P.	XX				
PR	29-OCT-1998;	98US-0106384P.	XX				
PR	29-OCT-1998;	98US-0108500P.	XX				
PR	30-OCT-1998;	98US-0106464P.	XX				
PR	03-NOV-1998;	98US-0106856P.	XX				
PR	03-NOV-1998;	98US-0106902P.	XX				
PR	03-NOV-1998;	98US-0106905P.	XX				
PR	03-NOV-1998;	98US-0106919P.	XX				
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PR	10-NOV-1998;	98US-0107753P.	XX				
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PR	18-NOV-1998;	98US-0108852P.	XX				
PR	18-NOV-1998;	98US-0108858P.	XX				
PR	18-NOV-1998;	98US-0108904P.	XX				
PR	22-DEC-1998;	98US-0113296P.	XX				
PR	30-DEC-1998;	98US-0114223P.	XX				
PR	05-JAN-1999;	99WO-US000106.	XX				
PR	16-APR-1999;	98US-0129674P.	XX				
PR	23-JUN-1999;	99US-0141037P.	XX				
PR	26-JUL-1999;	99US-0144758P.	XX				
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PR	15-SEP-1999;	99WO-US020111.	XX				
PR	29-OCT-1999;	99WO-US021194.	XX				
PR	29-OCT-1999;	98US-0162506P.	XX				
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PR	02-DEC-1999;	99WO-US028551.	XX				
PR	16-DEC-1999;	99WO-US030095.	XX				
PR	05-JAN-2000;	2000WO-US000219.	XX				
PR	06-JAN-2000;	2000WO-US000376.	XX				
PR	11-FEB-2000;	2000WO-US003565.	XX				
PR	18-FEB-2000;	2000WO-US004342.	XX				
PR	24-FEB-2000;	2000WO-US005004.	XX				
PR	02-MAR-2000;	2000WO-US005841.	XX				
PR	15-MAR-2000;	2000WO-US006884.	XX				
PR	17-MAY-2000;	2000WO-US013705.	XX				
PR	22-MAY-2000;	2000WO-US014042.	XX				
PR	30-MAY-2000;	2000WO-US014941.	XX				
PR	02-JUN-2000;	2000WO-US015264.	XX				
PR	23-AUG-2000;	2000WO-US023522.	XX				
PR	24-AUG-2000;	2000WO-US023328.	XX				
PR	08-NOV-2000;	2000WO-US030952.	XX				
PR	10-NOV-2000;	2000WO-US030873.	XX				
PR	01-DEC-2000;	2000WO-US032678.	XX				
PR	20-OCT-1998;	98US-0105002P.	PR	28-FEB-2001;	2001WO-US006520.	XX	(GETH) GENENTECH INC.
PR	21-OCT-1998;	98US-0105104P.	PR	01-MAR-2001;	2001WO-US006666.	XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Fertara N, Fong S;
PR	22-OCT-1998;	98US-0105159P.	PR	01-JUN-2001;	2001WO-US017800.	PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PR	22-OCT-1998;	98US-0105286P.	PR	20-JUN-2001;	2001WO-US019692.	PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PR	26-OCT-1998;	98US-0105693P.	PR	29-JUN-2001;	2001WO-US021066.	PI	Williams PW, Wood WI;
PR	26-OCT-1998;	98US-0105694P.	PR	09-JUL-2001;	2001WO-US021735.	XX	WPI; 2003-492259/46.
PR	27-OCT-1998;	98US-0105807P.	PR	04-SEP-2001;	2001US-00946374.	DR	P-PSDB; ABO44467.
PR	27-OCT-1998;	98US-0105881P.	XX			XX	Novel secreted and transmembrane polypeptides and polynucleotides
PR	27-OCT-1998;	98US-0106062P.	XX			PT	encoding them useful for treating various cardiac insufficiency
PR	28-OCT-1998;	98US-0106023P.	XX			PT	disorders, bone and/or cartilage disorders such as sports injuries and
PR	28-OCT-1998;	98US-0106030P.	XX			PT	arthritis.
PR	28-OCT-1998;	98US-0106032P.	DR				
PR	28-OCT-1998;	98US-0106178P.	DR				
PR	29-OCT-1998;	98US-0106248P.	XX				
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PR	30-OCT-1998;	98US-0106464P.	XX				
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PR	03-NOV-1998;	98US-0106919P.	XX				
PR	03-NOV-1998;	98US-0106932P.	XX				
PR	03-NOV-1998;	98US-0106934P.	XX				
PR	10-NOV-1998;	98US-0107753P.	XX				
PR	17-NOV-1998;	98US-0108775P.	XX				
PR	17-NOV-1998;	98US-0108779P.	XX				
PR	17-NOV-1998;	98US-0108867P.	XX				
PR	18-NOV-1998;	98US-0108925P.	XX				
PR	18-NOV-1998;	98US-0108848P.	XX				
PR	18-NOV-1998;	98US-0108849P.	XX				
PR	18-NOV-1998;	98US-0108850P.	XX				
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PR	22-DEC-1998;	98US-0113296P.	XX				
PR	30-DEC-1998;	98US-0114223P.	XX				
PR	05-JAN-1999;	99WO-US000106.	XX				
PR	16-APR-1999;	98US-0129674P.	XX				
PR	23-JUN-1999;	99US-0141037P.	XX				
PR	26-JUL-1999;	99US-0144758P.	XX				
PR	01-SEP-1999;	99US-0145698P.	XX				
PR	15-SEP-1999;	99WO-US020111.	XX				
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PR	30-NOV-1999;	99WO-US028311.	XX				
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PR	16-DEC-1999;	99WO-US030095.	XX				
PR	05-JAN-2000;	2000WO-US000219.	XX				
PR	06-JAN-2000;	2000WO-US000376.	XX				
PR	11-FEB-2000;	2000WO-US003565.	XX				
PR	18-FEB-2000;	2000WO-US004342.	XX				
PR	24-FEB-2000;	2000WO-US005004.	XX				
PR	02-MAR-2000;	2000WO-US005841.	XX				
PR	15-MAR-2000;	2000WO-US006884.	XX				
PR	17-MAY-2000;	2000WO-US013705.	XX				
PR	22-MAY-2000;	2000WO-US014042.	XX				
PR	30-MAY-2000;	2000WO-US014941.	XX				
PR	02-JUN-2000;	2000WO-US015264.	XX				
PR	23-AUG-2000;	2000WO-US023522.	XX				
PR	24-AUG-2000;	2000WO-US023328.	XX				
PR	08-NOV-2000;	2000WO-US030952.	XX				
PR	10-NOV-2000;	2000WO-US030873.	XX				
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Db 661 TATAACACCAAGCGCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAG 720
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Qy 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCGAGCTGGCCGAGCCAGCACATAC 900
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Qy 901 CTGGCCCTGGGAGGAAGCTGGCGATCTTCCGGAAGTACTTCGATGGACTCAACAG 960
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Qy 961 AAGGCCCGCGCGCCCGAGGCTGAGATGAGAGGTGGCCGAGGCTTGGGCTGAAAGT 1020
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Qy 1021 GCGGCCCTGGGCTTGAAGCTCCCTCTGTGAGGAGAGCCCTTCCCGAGTAACCT 1080
Db 1021 GCGGCCCTGGGCTTGAAGCTCCCTCTGTGAGGAGAGCCCTTCCCGAGTAACCT 1080
Qy 1081 CTGAGAGCAGATTGAAGCCAGGATGGCGCTCCAGACCCAGGACAGCTGCCCCATGC 1140
Db 1081 CTGAGAGCAGATTGAAGCCAGGATGGCGCTCCAGACCCAGGACAGCTGCCCCATGC 1140
Qy 1141 CGCGAGCTTCTGGCACTACTGAGCCGGGAGACCCAGGACTGGCGGCGCCATGCCGC 1200
Db 1141 CGCGAGCTTCTGGCACTACTGAGCCGGGAGACCCAGGACTGGCGGCGCCATGCCGC 1200
Qy 1201 AGTAGGTTCTAGGGGCGGTGCTGCGCCAGTGGACTGGCTGAGGAGAGCTGGCC 1260
Db 1201 AGTAGGTTCTAGGGGCGGTGCTGCGCCAGTGGACTGGCTGAGGAGAGCTGGCC 1260
Qy 1261 GGGCTCTGGCTGGTTCGGTCTGCTGTGCGCAGAGGGGAGGGCCATCTGATGTT 1320
Db 1261 GGGCTCTGGCTGGTTCGGTCTGCTGTGCGCAGAGGGGAGGGCCATCTGATGTT 1320
Qy 1321 CCCCTGGGAATCTAACTGGGAATGGCCAGGAGAGGGGCTGTGCACTTGCAGGCC 1380
Db 1321 CCCCTGGGAATCTAACTGGGAATGGCCAGGAGAGGGGCTGTGCACTTGCAGGCC 1380
Qy 1381 ACCTCAGGAGAGCCAGCGTGCCTGTGCGGAGGGTTCAGAGTCTCCGTAAGAGCAT 1440
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Qy 1441 GGGCAAGTTGCTGACACTTGTGATCTTGGTCCCTGTGGGACCTTGTGCATGATG 1500
Db 1441 GGGCAAGTTGCTGACACTTGTGATCTTGGTCCCTGTGGGACCTTGTGCATGATG 1500
Qy 1501 GTCTCTCTGAGCCCTGTTCTTCCAGAGTGAATGCTCAGATAAATGCTGTCTCCCA 1560
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Qy 1561 TGATGTTGGTACAGGAGCTGTTGCTGTGCTATGGCATGCTGTGCGGGGGTGTG 1620
Db 1561 TGATGTTGGTACAGGAGCTGTTGCTGTGCTATGGCATGCTGTGCGGGGGTGTG 1620
Qy 1621 CTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGAGAGTGCAGTGTCTATCCGAGTTC 1680
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RESULT 5

ACD67967

ID ACD67967 standard; cDNA; 1808 BP.

XX

AC ACD67967;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1430 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;

XX

OS tissue typing; chromosome identification; vaccine; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003073129-A1.

XX

PD 17-APR-2003.

XX

PF 04-SEP-2001; 2001US-00946374.

XX

PR 01-SEP-1998; 98US-0098716P.

PR

PR 01-SEP-1998; 98US-0098723P.

PR

PR 01-SEP-1998; 98US-0098749P.

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PR 01-SEP-1998; 98US-0098750P.

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PR 02-SEP-1998; 98US-0098803P.

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PR 02-SEP-1998; 98US-0098821P.

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PR 02-SEP-1998; 98US-0098843P.

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PR 09-SEP-1998; 98US-0099536P.

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PR 09-SEP-1998; 98US-0099596P.

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PR 09-SEP-1998; 98US-0099598P.

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PR 09-SEP-1998; 98US-0099642P.

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PR 10-SEP-1998; 98US-0099741P.

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PR 10-SEP-1998; 98US-0099763P.

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PR 10-SEP-1998; 98US-0099792P.

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PR 10-SEP-1998; 98US-0099808P.

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PR 10-SEP-1998; 98US-0099812P.

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PR 10-SEP-1998; 98US-0099815P.

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PR 10-SEP-1998; 98US-0099816P.

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PR 15-SEP-1998; 98US-0100385P.

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PR 15-SEP-1998; 98US-0100388P.

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PR 15-SEP-1998; 98US-0100390P.

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PR 15-SEP-1998; 98US-0100584P.

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PR 15-SEP-1998; 98US-0100862P.

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PR 15-SEP-1998; 98US-0100864P.

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PR 15-SEP-1998; 98US-0100863P.

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PR 15-SEP-1998; 98US-0100710P.

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PR 15-SEP-1998; 98US-0100711P.

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PR 15-SEP-1998; 98US-0100519P.

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PR 15-SEP-1998; 98US-0100530P.

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PR 15-SEP-1998; 98US-0100848P.

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PR 15-SEP-1998; 98US-0100849P.

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PR 15-SEP-1998; 98US-0101014P.

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PR 15-SEP-1998; 98US-0101068P.

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PR 15-SEP-1998; 98US-0101071P.

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PR 15-SEP-1998; 98US-0101279P.

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PR 15-SEP-1998; 98US-0101471P.

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PR 15-SEP-1998; 98US-0101472P.

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PR 15-SEP-1998; 98US-0101474P.

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PR 15-SEP-1998; 98US-0101475P.

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PR 15-SEP-1998; 98US-0101476P.

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PR 15-SEP-1998; 98US-0101477P.

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Db 61 GACGCTGTCCCGCGCGGCGATGAGCGGTACCTGTGCGGCTGTGCGGCTGGCAG 120
Qy 121 GTAGCAGCGCGCGCTGTCTCTCAAGAGCTATGTCAACGGTGGGGCTTGCCTCCAGCAAG 180
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Qy 181 GCCACCATCCCTGGGAAGACGGTCACTGTGACGGGCGCCAAACACAGCATCTGGGAAGCAG 240
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Qy 241 ACCGCTTGGAACTGGCCAGGAGAGGAGCAATCATCTGTGGCTCCCGAGACATGGAG 300
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Qy 301 AAGTGTAGGCGGAGCAAGGAATCATCGGGGAGACCTCAATCAACATGTCAACGCC 360
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Qy 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCGAGAGTTTGCAGCAAGATCATTTAA 420
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Qy 421 GAGGAGGAGCAGTGGACATTTAATCAACACCGGGGTGTGATCGGGTCCCGCACTGG 480
Db 421 GAGGAGGAGCAGTGGACATTTAATCAACACCGGGGTGTGATCGGGTCCCGCACTGG 480
Qy 481 ACCACCGAGGCGGCTTCGAGATCAGTTTGGCGTTAAACACCTGGGTCACTTCTCTTG 540
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Qy 541 ACAAACTGTCTGGCAAGCTGAAGCTTCAGCCCTTCGCGGATCATCAACCTCTCG 600
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Qy 601 TCCCTGGCCCATTTGTCTGGGCAATAGACTTTGACGACTTGAACCTGGCAGAGAGAG 660
Db 601 TCCCTGGCCCATTTGTCTGGGCAATAGACTTTGACGACTTGAACCTGGCAGAGAGAG 660
Qy 661 TATAACCAACAAAGCGGCTACTGCGAGGAGCTCGCCATCGTCCTTTACCAAGGAG 720
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Qy 781 AGGACAGGCTGGGAGACACAGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC 840
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Qy 961 AAGGCCCGGCGCCCGAGGCTGAGATGAGAGGTGGCCCGGAGGCTTTGGGCTGAAAGT 1020
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Qy 1081 CTGAGAGCAGATTGAAGCCAGGATGGCGCTCCAGACCGAGGACAGTGTCCGCCATGC 1140
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Qy 1741 CTGGGACTCCCACTTCTATCAATCTCATGGTAGTCCAACTGCAGACTCTCAAACTT 1800
Db 1741 CTGGGACTCCCACTTCTATCAATCTCATGGTAGTCCAACTGCAGACTCTCAAACTT 1800
Qy 1801 GCTCATTT 1808
Db 1801 GCTCATTT 1808
RESULT 6
ADC17984
ID ADC17984 standard; cDNA; 1808 BP.
XX
AC ADC17984;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO polynucleotide #33.
XX
KW Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;
XX gene mapping; genetic disorder.
OS Homo sapiens.
XX
PN US2003064925-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00013907.
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PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103385P.
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PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104967P.
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PR 20-OCT-1998; 98US-0105002P.
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PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107753P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 22-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99WO-US020111.
PR 01-SEP-1999; 99WO-US021194.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006656.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021086.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Borstein D, Deanovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoletti NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-555602/52.
DR P-PSDB; ADC17985.
XX
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Claim 2; SEQ ID NO 115; 555pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The sequences are useful in the preparation of a
CC medicament for treating a condition responsive to a PRO polypeptide. The
CC polypeptides are useful in a number of functional biological assays, as
CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 1808; DB 9; Length 1808;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAGCGCTGTCCCGCGCGCGATGACGCGTACCTGTCGCGCTGTGCGCGCTGGGACG 120
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				PR	07-OCT-1998;	98US-0103315P.
				PR	07-OCT-1998;	98US-0103328P.
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				PR	26-OCT-1998;	98US-0105694P.
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				PR	17-NOV-1998;	98US-0108779P.

RESULT 7
ADD70630
ID ADD70630 standard; cDNA; 1808 BP.
XX AC
AC ADD70630;
XX DT
15-JAN-2004 (first entry)
Human cDNA encoding secreted/transmembrane protein PRO1430.
XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX OS
Homo sapiens.
XX US2003099625-A1.
XX 29-MAY-2003.
XX 12-DEC-2001; 2001US-00015386.
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.

QY 1081 CTGGACGATTTAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140
PD |||||
XX 1081 CTGGACGATTTAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140
PF |||||
XX 1141 CCGCAGCTTCTGGGCACTACCTGAGCCGGGAGACCCAGGACTGGGGCCCATCCCGC 1200
PR |||||
XX 1141 CCGCAGCTTCTGGGCACTACCTGAGCCGGGAGACCCAGGACTGGGGCCCATCCCGC 1200
PR |||||
QY 1201 AGTAGGTTCTAGGGGCGGCTGGCGGAGTGAGTGGCTTGCAGGTGAGCACTGCCCC 1260
DB |||||
QY 1201 AGTAGGTTCTAGGGGCGGCTGGCGGAGTGAGTGGCTTGCAGGTGAGCACTGCCCC 1260
DB |||||
QY 1261 GGGCTCTGGCTGTTCCGTCGCTCTGCTGCTGCCAGAGGGGAGGGGCCATCTGATGTT 1320
DB |||||
QY 1261 GGGCTCTGGCTGTTCCGTCGCTCTGCTGCTGCCAGAGGGGAGGGGCCATCTGATGTT 1320
DB |||||
QY 1321 CCCTCGGATCTAACTGGGAATGCGGAGGAGGAGGGCTCTGTGCACTTGCAAGGC 1380
DB |||||
QY 1321 CCCTCGGATCTAACTGGGAATGCGGAGGAGGAGGGCTCTGTGCACTTGCAAGGC 1380
DB |||||
QY 1381 ACCTCAGGAGCCAGCGGTGCTGCTGGGGAGGGTTCCAAAGTGTCTCGTGGAAGCAT 1440
DB |||||
QY 1381 ACCTCAGGAGCCAGCGGTGCTGCTGGGGAGGGTTCCAAAGTGTCTCGTGGAAGCAT 1440
DB |||||
QY 1441 GGGCAAGTGTCTGACACTTGGTGGATCTTGGTGGTCTCTGCGGAGCTTGTGCACTG 1500
DB |||||
QY 1441 GGGCAAGTGTCTGACACTTGGTGGATCTTGGTGGTCTCTGCGGAGCTTGTGCACTG 1500
DB |||||
QY 1501 GTCTCTCTGAGCCTTGGTTTCTTTCAGCACTGAGTGTCTGCAATTAAGTGTCTCCCA 1560
DB |||||
QY 1501 GTCTCTCTGAGCCTTGGTTTCTTTCAGCACTGAGTGTCTGCAATTAAGTGTCTCCCA 1560
DB |||||
QY 1561 TGATGTTGTTGACAGGAGCTGTGCTGCTGCTATGCTGCTGCTGCTGCTGCTGCTG 1620
DB |||||
QY 1561 TGATGTTGTTGACAGGAGCTGTGCTGCTGCTATGCTGCTGCTGCTGCTGCTGCTG 1620
DB |||||
QY 1621 CTGAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB |||||
QY 1621 CTGAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB |||||
QY 1681 AGGCTCTGACGGATGGAGTGGGAACCCACAGCTGCTGCTACAGGACTGGGATTGC 1740
DB |||||
QY 1681 AGGCTCTGACGGATGGAGTGGGAACCCACAGCTGCTGCTACAGGACTGGGATTGC 1740
DB |||||
QY 1741 CTGGGACTCCCACTTCTCTATCAATTTCTATGTTAGTCCAACTGCAAGCTCTCAAACT 1800
DB |||||
QY 1741 CTGGGACTCCCACTTCTCTATCAATTTCTATGTTAGTCCAACTGCAAGCTCTCAAACT 1800
DB |||||
QY 1801 GCTCATTT 1808
DB |||||
QY 1801 GCTCATTT 1808
DB |||||

RESULT 8
ADD39707
ID ADD39707 standard; cDNA; 1808 BP.
XX
AC ADD39707;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1430.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
OS Homo sapiens.
XX
PN US2003083462-A1.

XX 01-MAY-2003.
PD 10-DEC-2001; 2001US-00013913.
XX 05-JAN-1999; 99WO-US0001106.
PR 01-SEP-1999; 99WO-US0201111.
PR 15-SEP-1999; 99WO-US021194.
PR 30-NOV-1999; 99WO-US028113.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023322.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019892.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
PA Baker KP, Botstein D, Deanyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI: 2003-755122/71.
DR P-PSDB; ADD39708.
XX
XX New secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX Claim 2; SEQ ID NO 115; 557pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimaeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. PRO is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1245
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for stimulating calcium flux in human
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders

23-JUN-1999; 99US-0141037P.
 20-JUL-1999; 99US-0144758P.
 26-JUL-1999; 99US-0145698P.
 01-SEP-1999; 99WO-US020111.
 15-SEP-1999; 99WO-US021194.
 29-OCT-1999; 99US-0162506P.
 30-NOV-1999; 99WO-US028313.
 02-DEC-1999; 99WO-US028551.
 16-DEC-1999; 99WO-US031095.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000376.
 11-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004342.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 15-MAR-2000; 2000WO-US013705.
 17-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000WO-US030952.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 04-SEP-2001; 2001US-00946374.
 (GETH) GENENTECH INC.
 Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 Williams EM, Wood WI;
 WPI; 2003-708344/67.
 P-PSDB; ADD70154.
 Novel isolated PRO polypeptide useful for tissue typing, modulating
 biological activity of cell, as molecular weight markers in protein
 electrophoresis, for treating arthritis, tumor.
 Claim 2; SEQ ID NO 115; 549pp; English.
 The invention relates to an isolated PRO polypeptide (secreted or
 Query Match 100.0%; Score 1808; DB 9; Length 1808;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGTACCCAGCGCGCTGGTGTGACGAAGTCCGCGCGGACTCCGAGCGCTGACGCCT 60
 Db 1 GAGTACCCAGCGCGCTGGTGTGACGAAGTCCGCGCGGACTCCGAGCGCTGACGCCT 60
 QY 61 GACGCTGTCCCGGCCCGCATGAGCGCTACCTGCTGCGCTGTGGCGCTGGGCACG 120
 Db 61 GACGCTGTCCCGGCCCGCATGAGCGCTACCTGCTGCGCTGTGGCGCTGGGCACG 120
 QY 121 GTAGAGGCGCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCGCAAG 180
 Db 121 GTAGAGGCGCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCGCAAG 180
 QY 181 GCCACATCCCTGGGAAGACGGTCTCTGTCGCGCGCCCAACACAGGCATCGGAAGCAG 240
 Db 181 GCCACATCCCTGGGAAGACGGTCTCTGTCGCGCGCCCAACACAGGCATCGGAAGCAG 240
 QY 241 ACCGCTTGGAACTGGCCAGGAGAGGAGGCAACATCATCTTGGCTGCGGAGACATGGAG 300

Db 241 ACCGCTTGGAACTGGCCAGGAGAGGAGCAACATCATCTTGGCTGCGGAGACATGGAG 300
 QY 301 AAGTGTGAGGCGGAGCAAAAGACATCCGCGGGAGAGCCCTCAATCACCATTGTCAACGCC 360
 Db 301 AAGTGTGAGGCGGAGCAAAAGACATCCGCGGGAGAGCCCTCAATCACCATTGTCAACGCC 360
 QY 361 CGGCACTTGGCACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAATCATTTGAA 420
 Db 361 CGGCACTTGGCACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAATCATTTGAA 420
 QY 421 GAGGAGGAGCGAGTGGACATTTCTATCAACCAACGCGGTGTATGCGGTGCCCCACTGG 480
 Db 421 GAGGAGGAGCGAGTGGACATTTCTATCAACCAACGCGGTGTATGCGGTGCCCCACTGG 480
 QY 481 ACCACCGAGGACGGCTTCCGAGATGCAAGTTTGGCGTTAAACACCTGGGTCACTTTCTTTG 540
 Db 481 ACCACCGAGGACGGCTTCCGAGATGCAAGTTTGGCGTTAAACACCTGGGTCACTTTCTTTG 540
 QY 541 ACACACTTGTCTGCTGGACAAAGCTGAAGCTGAAGCCCTGAGCCCTTCCGGATCATCAACTCTCG 600
 Db 541 ACACACTTGTCTGCTGGACAAAGCTGAAGCTGAAGCCCTTCCGGATCATCAACTCTCG 600
 QY 601 TCCCTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTTGAACTGGCAGACGAGGAAG 660
 Db 601 TCCCTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTTGAACTGGCAGACGAGGAAG 660
 QY 661 TATAACACCAAGCGCGCTACTGCGAGAGCAAGCTCGGCATCGCTCTTCCACCAAGAG 720
 Db 661 TATAACACCAAGCGCGCTACTGCGAGAGCAAGCTCGGCATCGCTCTTCCACCAAGAG 720
 QY 721 CTGAGCCGCGCGCTGCAAGGCTCTGGTGTGACTGTCTCAACGCGCTGACCCCGGCTGCCC 780
 Db 721 CTGAGCCGCGCGCTGCAAGGCTCTGGTGTGACTGTCTCAACGCGCTGACCCCGGCTGCCC 780
 QY 781 AGGACAGAGCTGGGAGACACACCGGCGATCATGGCTTCCCTTCCAGCAGCACACATC 840
 Db 781 AGGACAGAGCTGGGAGACACACCGGCGATCATGGCTTCCCTTCCAGCAGCACACATC 840
 QY 841 GGGCCCATCTTCTGCTGCTGCTCAAGAGCCCGAGCTGGCGCGCCAGCCAGCCAGCACATAC 900
 Db 841 GGGCCCATCTTCTGCTGCTGCTCAAGAGCCCGAGCTGGCGCGCCAGCCAGCCAGCACATAC 900
 QY 901 CTGGCGCTGGGAGGAACTGGCGGATGTTTCCGAAAAGTACTTCGATGGACTCAAAAG 960
 Db 901 CTGGCGCTGGGAGGAACTGGCGGATGTTTCCGAAAAGTACTTCGATGGACTCAAAAG 960
 QY 961 AAGGCCCGCGCGCCCGAGGCTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGT 1020
 Db 961 AAGGCCCGCGCGCCCGAGGCTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGT 1020
 QY 1021 GCGCGCTGGTGGCTTAGAGGCTCCCTCTGTGAGGAGGAGCCCTTCCCGAGATAACCT 1080
 Db 1021 GCGCGCTGGTGGCTTAGAGGCTCCCTCTGTGAGGAGGAGCCCTTCCCGAGATAACCT 1080
 QY 1081 CTGGAGCATTTGAAAGCCAGGATGGCGCTCCAGACCGAGGAGAGCTGTCCGCGCATGC 1140
 Db 1081 CTGGAGCATTTGAAAGCCAGGATGGCGCTCCAGACCGAGGAGAGCTGTCCGCGCATGC 1140
 QY 1141 CCGCAGCTTCTGGCACTACCTGAGCCGAGAGACCCAGACTGGCGCGCCCATGCCCCGC 1200
 Db 1141 CCGCAGCTTCTGGCACTACCTGAGCCGAGAGACCCAGACTGGCGCGCCCATGCCCCGC 1200
 QY 1201 AGTAGATTCTAGGGGCGGTGCTGGCCGAGTGGACTGSCCTGAGGTGAGCACTGCCCC 1260
 Db 1201 AGTAGATTCTAGGGGCGGTGCTGGCCGAGTGGACTGSCCTGAGGTGAGCACTGCCCC 1260
 QY 1261 GGGCTCTGGCTGGTTCCGCTCTGCTCTGTGCGCAGAGGGAGAGGGCCCATCTGATGCTT 1320
 Db 1261 GGGCTCTGGCTGGTTCCGCTCTGCTCTGTGCGCAGAGGGAGAGGGCCCATCTGATGCTT 1320
 QY 1321 CCCTTGGGAATCTAAACTGGGAATGGCCGAGGAGAGGGGCTCTGTGACATTGAGGCGC 1380
 Db 1321 CCCTTGGGAATCTAAACTGGGAATGGCCGAGGAGAGGGGCTCTGTGACATTGAGGCGC 1380

QY	1381	ACGTCAGAGAGCCAGCGTGCCTCTCGGGGAGGTTTCAAGGTCTCCGTGAAGAGCAT	1440	PR	10-SEP-1998;	98US-0099763P.
Db	1381	ACGTCAGAGAGCCAGCGTGCCTCTCGGGGAGGTTTCAAGGTCTCCGTGAAGAGCAT	1440	PR	10-SEP-1998;	98US-0099792P.
QY	1441	GGCAGATTGTGTGACACTTGGTGTGATCTTGGTCCCTGTGGGACCTTGTGCATGCATG	1500	PR	10-SEP-1998;	98US-0099808P.
Db	1441	GGCAGATTGTGTGACACTTGGTGTGATCTTGGTCCCTGTGGGACCTTGTGCATGCATG	1500	PR	10-SEP-1998;	98US-0099812P.
QY	1501	GTCTCTCTGAGCCCTTGTTCTTCCAGCAGTGCAGATGCTCAGAAATGCTGTCTCCCA	1560	PR	10-SEP-1998;	98US-0099815P.
Db	1501	GTCTCTCTGAGCCCTTGTTCTTCCAGCAGTGCAGATGCTCAGAAATGCTGTCTCCCA	1560	PR	10-SEP-1998;	98US-0099816P.
QY	1561	TGATGTGTGTACAGCAGCTGTGTCTGGCTATGGCATGCTGCGGGGGTGTG	1620	PR	10-SEP-1998;	98US-0100385P.
Db	1561	TGATGTGTGTGTACAGCAGCTGTGTCTGGCTATGGCATGCTGCGGGGGTGTG	1620	PR	10-SEP-1998;	98US-0100388P.
QY	1621	CTGAGGCTCTCTGTGCCAGAGCCAGCCAGCAGTGCAGTGTGTCATCCCGAGTTC	1680	PR	10-SEP-1998;	98US-0100390P.
Db	1621	CTGAGGCTCTCTGTGCCAGAGCCAGCCAGCAGTGCAGTGTGTCATCCCGAGTTC	1680	PR	10-SEP-1998;	98US-0100384P.
QY	1681	AGGCTCTGACGGCATGGATGGGACCCAGCCAGCTGCTGACAGCCTGGGATTGC	1740	PR	10-SEP-1998;	98US-0100662P.
Db	1681	AGGCTCTGACGGCATGGATGGGACCCAGCCAGCTGCTGACAGCCTGGGATTGC	1740	PR	10-SEP-1998;	98US-0100683P.
QY	1741	CTGGGACTCCCACTTCCTATCAATTTCTCATGTTAGTCCAAACTGCAGACTCTCAAACCT	1800	PR	10-SEP-1998;	98US-0100684P.
Db	1741	CTGGGACTCCCACTTCCTATCAATTTCTCATGTTAGTCCAAACTGCAGACTCTCAAACCT	1800	PR	10-SEP-1998;	98US-0100710P.
QY	1801	GCTCATTT 1808		PR	10-SEP-1998;	98US-0100711P.
Db	1801	GCTCATTT 1808		PR	10-SEP-1998;	98US-0100719P.
RESULT 10						
ADD38274						
ID	ADD38274	standard; cDNA; 1808 BP.				
XX	AC					
XX	AC					
XX	AC					
DT	15-JAN-2004	(first entry)				
XX	DE	Human cDNA encoding secreted/transmembrane protein PRO1430.				
XX	XX	Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;				
KW	XX	immune response; cardiac insufficiency disorder; calcium flux;				
KW	XX	umbilical vein endothelial cell; bone disorder; cartilage disorder;				
KW	XX	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;				
KW	XX	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;				
KW	XX	dermatitis; herpeticiformis; Crohn's disease; thalassemia.				
OS	XX	Homo sapiens.				
XX	XX					
FN	US2003096955-A1.					
XX	XX					
PD	22-MAY-2003.					
XX	XX					
PF	07-DEC-2001; 2001US-00012755.					
XX	XX					
PR	01-SEP-1998;	98US-0098716P.				
PR	01-SEP-1998;	98US-0098723P.				
PR	01-SEP-1998;	98US-0098749P.				
PR	01-SEP-1998;	98US-0098750P.				
PR	02-SEP-1998;	98US-0098803P.				
PR	02-SEP-1998;	98US-0098821P.				
PR	02-SEP-1998;	98US-0098843P.				
PR	03-SEP-1998;	98US-0098936P.				
PR	09-SEP-1998;	98US-0099596P.				
PR	09-SEP-1998;	98US-0099598P.				
PR	09-SEP-1998;	98US-0099602P.				
PR	09-SEP-1998;	98US-0099642P.				
PR	10-SEP-1998;	98US-0099741P.				
PR	10-SEP-1998;	98US-0099754P.				

PR	27-OCT-1998;	98US-0106062P.	XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PR	28-OCT-1998;	98US-0106023P.	PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PR	28-OCT-1998;	98US-0106029P.	PI	Pan J, Pacini NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PR	28-OCT-1998;	98US-0106030P.	PI	Williams PW, Wood WI;
PR	28-OCT-1998;	98US-0106032P.	XX	WPI: 2003-787000/74.
PR	28-OCT-1998;	98US-0106117P.	DR	P-PSDB; ADD38275.
PR	29-OCT-1998;	98US-0106248P.	DR	
PR	29-OCT-1998;	98US-0106384P.	XX	Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PR	29-OCT-1998;	98US-0108500P.	PT	cardiac insufficiency disorders, wound healing, diabetes mellitus,
PR	30-OCT-1998;	98US-0106464P.	PT	thalassemias.
PR	03-NOV-1998;	98US-0106856P.	XX	
PR	03-NOV-1998;	98US-0106902P.	XX	Claim 2; SEQ ID NO 115; 556pp; English.
PR	03-NOV-1998;	98US-0106905P.	XX	
PR	03-NOV-1998;	98US-0106912P.	XX	
PR	03-NOV-1998;	98US-0106934P.	XX	
PR	10-NOV-1998;	98US-0107783P.	CC	The invention relates to an isolated PRO polypeptide (secreted or
PR	17-NOV-1998;	98US-0108775P.	CC	transmembrane protein) having at least 80% amino acid sequence identity
PR	17-NOV-1998;	98US-0108779P.		
PR	17-NOV-1998;	98US-0108787P.		
PR	17-NOV-1998;	98US-0108788P.		
PR	17-NOV-1998;	98US-0108801P.		
PR	17-NOV-1998;	98US-0108802P.		
PR	17-NOV-1998;	98US-0108806P.		
PR	17-NOV-1998;	98US-0108807P.		
PR	17-NOV-1998;	98US-0108867P.		
PR	17-NOV-1998;	98US-0108925P.		
PR	18-NOV-1998;	98US-0108848P.		
PR	18-NOV-1998;	98US-0108849P.		
PR	18-NOV-1998;	98US-0108850P.		
PR	18-NOV-1998;	98US-0108851P.		
PR	18-NOV-1998;	98US-0108852P.		
PR	18-NOV-1998;	98US-0108904P.		
PR	22-DEC-1998;	98US-0113296P.		
PR	30-DEC-1998;	98US-0114223P.		
PR	05-JAN-1999;	99WO-US000106.		
PR	16-APR-1999;	99US-0129674P.		
PR	23-JUN-1999;	99US-0141037P.		
PR	26-JUL-1999;	99US-0144758P.		
PR	20-AUG-1999;	99US-0145698P.		
PR	01-SEP-1999;	99WO-US020111.		
PR	15-SEP-1999;	99WO-US021134.		
PR	29-OCT-1999;	99US-0162508P.		
PR	30-NOV-1999;	99WO-US028313.		
PR	02-DEC-1999;	99WO-US028551.		
PR	16-DEC-1999;	99WO-US030095.		
PR	05-JAN-2000;	2000WO-US000219.		
PR	06-JAN-2000;	2000WO-US000376.		
PR	11-FEB-2000;	2000WO-US0003565.		
PR	18-FEB-2000;	2000WO-US004342.		
PR	24-FEB-2000;	2000WO-US005004.		
PR	02-MAR-2000;	2000WO-US005841.		
PR	15-MAR-2000;	2000WO-US006884.		
PR	17-MAY-2000;	2000WO-US013705.		
PR	22-MAY-2000;	2000WO-US014042.		
PR	30-MAY-2000;	2000WO-US014941.		
PR	02-JUN-2000;	2000WO-US015284.		
PR	23-AUG-2000;	2000WO-US023522.		
PR	24-AUG-2000;	2000WO-US023328.		
PR	08-NOV-2000;	2000WO-US030952.		
PR	10-NOV-2000;	2000WO-US030873.		
PR	01-DEC-2000;	2000WO-US032678.		
PR	28-FEB-2001;	2001WO-US006520.		
PR	01-MAR-2001;	2001WO-US006866.		
PR	01-JUN-2001;	2001WO-US017800.		
PR	20-JUN-2001;	2001WO-US019692.		
PR	29-JUN-2001;	2001WO-US021066.		
PR	09-JUL-2001;	2001WO-US021735.		
PR	04-SEP-2001;	2001US-00946374.		
XX				
PA	(GETH) GENENTECH INC.			

781 AGGACAGCTGGGACAGACACAGGGGATCCATGCTCCACCTTCTCAGACACCACTC 840
 Db |
 781 AGGACAGCTGGGACAGACACAGGGGATCCATGCTCCACCTTCTCAGACACCACTC 840
 Qy |
 841 GGGCCCATCTTCTGGCTGTGTGTTCAAGAGCCCGAGCTGGCCGCGCCAGCCAGCACATAC 900
 Db |
 841 GGGCCCATCTTCTGGCTGTGTGTTCAAGAGCCCGAGCTGGCCGCGCCAGCCAGCACATAC 900
 Qy |
 901 CTGGCCGTGGGAGGAACTGGCGGATGTTTCGGAAAGTACTTCGATGAGCTCAAAACAG 960
 Db |
 901 CTGGCCGTGGGAGGAACTGGCGGATGTTTCGGAAAGTACTTCGATGAGCTCAAAACAG 960
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 961 AAGGCCCGCCCGCCCGAGCTGAGGATGAGGAGTGGCCGCGAGGCTTGGCTGAAAGT 1020
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 961 AAGGCCCGCCCGCCCGAGCTGAGGATGAGGAGTGGCCGCGAGGCTTGGCTGAAAGT 1020
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 1081 CTGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCGAGACAGCTGTCCGCCATGC 1140
 Db |
 1081 CTGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCGAGACAGCTGTCCGCCATGC 1140
 Qy |
 1141 CCGCAGCTTCTGGCACTACTGAGCGGGAGACCCAGAGCTGGCGCGCCATGCCGCG 1200
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 1141 CCGCAGCTTCTGGCACTACTGAGCGGGAGACCCAGAGCTGGCGCGCCATGCCGCG 1200
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 Db |
 1201 AGTAGGTTCTAGGGGGCGGCTGGCGCAGTGGAGTGGCTGAGCTGAGCAGTGCCTCC 1260
 Qy |
 1261 GGGCTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 Db |
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 1381 ACGTGAGAGCCAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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 Qy |
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 Qy |
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 Db |
 1801 GCTCATTT 1808

RESULT 11
 ADD39230
 ID ADD39230 standard; cDNA; 1808 BP.
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 AC ADD39230;
 XX
 DT 15-JAN-2004 (first entry)
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 DE Human cDNA encoding secreted/transmembrane protein PRO1430.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003096954-A1.
 XX
 PD 22-MAY-2003.
 XX
 PF 07-DEC-2001; 2001US-00011671.
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 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 02-SEP-1998; 98US-0098536P.
 PR 09-SEP-1998; 98US-0099596P.
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 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
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 PR 15-SEP-1998; 98US-0100385P.
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 PR 17-SEP-1998; 98US-0100935P.
 PR 18-SEP-1998; 98US-0100848P.
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 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101069P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
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 PR 23-SEP-1998; 98US-0101476P.
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PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	PR	22-DEC-1998;	98US-0113298P.
PR	24-SEP-1998;	98US-0101916P.	PR	30-DEC-1998;	98US-0114223P.
PR	29-SEP-1998;	98US-0102207P.	PR	05-JAN-1999;	99WO-US000106.
PR	29-SEP-1998;	98US-0102240P.	PR	16-APR-1999;	99US-0129674P.
PR	29-SEP-1998;	98US-0102307P.	PR	23-JUN-1999;	99US-0141037P.
PR	29-SEP-1998;	98US-0102330P.	PR	20-JUL-1999;	99US-0144758P.
PR	29-SEP-1998;	98US-0102331P.	PR	26-JUL-1999;	99US-0145698P.
PR	30-SEP-1998;	98US-0102484P.	PR	01-SEP-1999;	99WO-US020111.
PR	30-SEP-1998;	98US-0102487P.	PR	15-SEP-1999;	99WO-US021194.
PR	30-SEP-1998;	98US-0102570P.	PR	29-OCT-1999;	99US-0162506P.
PR	30-SEP-1998;	98US-0102571P.	PR	30-NOV-1999;	99WO-US028313.
PR	01-OCT-1998;	98US-0102687P.	PR	02-DEC-1999;	99US-02028551.
PR	01-OCT-1998;	98US-0102687P.	PR	16-DEC-1999;	99WO-US030095.
PR	02-OCT-1998;	98US-0102965P.	PR	05-JAN-2000;	2000WO-US000219.
PR	06-OCT-1998;	98US-0103258P.	PR	06-JAN-2000;	2000WO-US000376.
PR	06-OCT-1998;	98US-0103449P.	PR	11-FEB-2000;	2000WO-US003585.
PR	07-OCT-1998;	98US-0103314P.	PR	18-FEB-2000;	2000WO-US004342.
PR	07-OCT-1998;	98US-0103315P.	PR	24-FEB-2000;	2000WO-US005004.
PR	07-OCT-1998;	98US-0103328P.	PR	02-MAR-2000;	2000WO-US005841.
PR	07-OCT-1998;	98US-0103398P.	PR	15-MAR-2000;	2000WO-US006884.
PR	07-OCT-1998;	98US-0103396P.	PR	17-MAY-2000;	2000WO-US013705.
PR	07-OCT-1998;	98US-0103401P.	PR	22-MAY-2000;	2000WO-US014042.
PR	08-OCT-1998;	98US-0103633P.	PR	30-MAY-2000;	2000WO-US014941.
PR	08-OCT-1998;	98US-0103678P.	PR	02-JUN-2000;	2000WO-US015284.
PR	08-OCT-1998;	98US-0103679P.	PR	23-AUG-2000;	2000WO-US023522.
PR	14-OCT-1998;	98US-0103711P.	PR	24-AUG-2000;	2000WO-US023328.
PR	20-OCT-1998;	98US-0104257P.	PR	08-NOV-2000;	2000WO-US030952.
PR	20-OCT-1998;	98US-0104987P.	PR	10-NOV-2000;	2000WO-US030873.
PR	20-OCT-1998;	98US-0105000P.	PR	01-DEC-2000;	2000WO-US032678.
PR	20-OCT-1998;	98US-0105002P.	PR	28-FEB-2001;	2001WO-US006520.
PR	21-OCT-1998;	98US-0105104P.	PR	01-MAR-2001;	2001WO-US006666.
PR	22-OCT-1998;	98US-0105169P.	PR	01-JUN-2001;	2001WO-US017800.
PR	22-OCT-1998;	98US-0105266P.	PR	20-JUN-2001;	2001WO-US019692.
PR	26-OCT-1998;	98US-0105693P.	PR	29-JUN-2001;	2001WO-US021066.
PR	26-OCT-1998;	98US-0105694P.	PR	09-JUL-2001;	2001WO-US021735.
PR	27-OCT-1998;	98US-0105807P.	PR	04-SEP-2001;	2001US-00946374.
PR	27-OCT-1998;	98US-0105881P.	XX		
PR	27-OCT-1998;	98US-0105882P.	PA	(GETH) GENENTECH INC.	
PR	27-OCT-1998;	98US-0106062P.	XX		
PR	28-OCT-1998;	98US-0106023P.	PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,	
PR	28-OCT-1998;	98US-0106029P.	PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;	
PR	28-OCT-1998;	98US-0106030P.	PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tunas D, Watanabe CK;	
PR	28-OCT-1998;	98US-0106032P.	PI	Williams PM, Wood WI;	
PR	28-OCT-1998;	98US-0106033P.	XX		
PR	29-OCT-1998;	98US-0106248P.	DR	WPI; 2003-786999/74.	
PR	29-OCT-1998;	98US-0106384P.	DR	P-PSDB; ADD39231.	
PR	29-OCT-1998;	98US-0106500P.	XX		
PR	30-OCT-1998;	98US-0106464P.	PT	Novel isolated PRO polypeptide useful for tissue typing, modulating	
PR	03-NOV-1998;	98US-0106856P.	PT	biological activity of cell, as molecular weight markers in protein	
PR	03-NOV-1998;	98US-0106902P.	PT	electrophoresis, for treating arthritis, tumor.	
PR	03-NOV-1998;	98US-0106905P.	XX		
PR	03-NOV-1998;	98US-0106919P.	XX	Claim 2; SEQ ID NO 115; 550pp; English.	
PR	03-NOV-1998;	98US-0106932P.	XX	The invention relates to an isolated PRO polypeptide (secreted or	
PR	03-NOV-1998;	98US-0106934P.	XX		
PR	10-NOV-1998;	98US-0107783P.	Query Match	100.0%; Score 1808; DB 9; Length 1808;	
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PR	17-NOV-1998;	98US-0108807P.	QY	61 GAGCGCTGTCCCGCGCGCATGAGCGCTACCTGCTGCCGCTGTGCGCGCTGGGACG	120
PR	17-NOV-1998;	98US-0108867P.	Db	61 GAGCGCTGTCCCGCGCGCATGAGCGCTACCTGCTGCCGCTGTGCGCGCTGGGACG	120
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PR	18-NOV-1998;	98US-0108849P.	Db	121 GTAGCAGGCGCGCGCTGTGTGTCAGGACTATGTACCGGTGGGCTTCCCCCGACG	180

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 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCGAGCTGGCCGCCAGCCAGCACATAC 900
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 1021 GCGCGCTGGTGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCCGCATACCT 1080
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 1621 CTGAGGGCTTCTGTCGAGAGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
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 1801 GCTCAATTT 1808
 1801 GCTCAATTT 1808

RESULT 12
 ADD38753
 ID ADD38753 standard; cDNA; 1808 BP.
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 AC ADD38753;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO1430.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003092061-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 06-DEC-2001; 2001US-00007194.
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 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.

PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PW, Wood WI;
XX WPI; 2003-765477/72.
DR P-PSDB; ADD38754.
XX
XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, useful for treating cancerous tumors, cardiac
PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.
XX Claim 2; SEQ ID NO 115; 555pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1808; DB 9; Length 1808;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTACCCAGGCGGTGTGTGTCAGCAAGCTCCGCGGACTCCGGAGCGCTGACGCT 60
DB 1 GAGTACCCAGGCGGTGTGTGTCAGCAAGCTCCGCGGACTCCGGAGCGCTGACGCT 60
QY 61 GAGCGCTGTCCCGCGCGCATGAGCGCTACCTGCTCCGCTGTCCGCGTGGGACG 120
DB 61 GAGCGCTGTCCCGCGCGCATGAGCGCTACCTGCTCCGCTGTCCGCGTGGGACG 120
QY 121 GTAGCAGGCGCCCGTGTGTCTCAAGAGCTATGTCAACGCGTGGGCTTGGCCAGCAAG 180
DB 121 GTAGCAGGCGCCCGTGTGTCTCAAGAGCTATGTCAACGCGTGGGCTTGGCCAGCAAG 180
QY 181 GCCACCATCCCTGGGAGAGCGTCATGTGACGGGCGCCCAACACAGGCTCGGAGCAG 240
DB 181 GCCACCATCCCTGGGAGAGCGTCATGTGACGGGCGCCCAACACAGGCTCGGAGCAG 240
QY 241 ACCGCTTGAACTGGCCAGAGAGGAGCAACATCATCTGCGCTCGCGAGACATGGAG 300
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QY 421 GAGGAGAGCGAGTGGACATTTAATAACAAACCGCGGTGTGATGCGGTGCCCGCACTGG 480
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DB 481 ACCACCGAGAGCGCTTCGAGATGCGAGTTGGCGTTAAACCACTGGGTCACTTCTCTTG 540
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DB 601 TCCCTGCGCCATGTCTGGGCAATAGACTTTGACGACTTGAACCTGGCAGAGGAG 660

QY 661 TATAACACCAAGCCGCTACTGCCAGACCAAGCTGCGCATCGTCTCTTCCACCAAGGAG 720
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DB 721 CTGAGCGGCGGCTGCAAGGCTCTGTGTGACTGTCAACGCGCTGCAACCGCGCTGGCC 780
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QY 901 CTGCGCGTGGCGAGGAATGCGGATGTTCCGGAAGTACTTTCAGTGAATCAACAG 960
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DB 1021 GCGCGCTGTGTGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCGCCCTCCCGAGATAACCT 1080
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DB 1081 CTGAGCAGAGATTTGAAAGCCAGGATGCGCGCTCCACACCGAGACAGCTGTCCGCCATGC 1140
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XX AC ADD40184;
XX DT 15-JAN-2004 (first entry)
XX DE Human cDNA encoding secreted/transmembrane protein PRO1430.
XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX OS Homo sapiens.
XX PN US2003082627-A1.
XX PD 01-MAY-2003.
XX PF 06-DEC-2001; 2001US-00006117.
XX PR 01-SEP-1998; 98US-0098716P.
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PR 09-JUL-2001; 2001MO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-755104/71.
XX P-PSDB; ADD40185.
XX
PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.
XX
PS Claim 2; SEQ ID NO 115; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1808; DB 9; Length 1808;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGCGCGTGGTGTGAGCAAGCTCCGCGCCGACTCCGAGCCCTGAGCCCT 60
DB 1 GAGCTACCCAGCGCGTGGTGTGAGCAAGCTCCGCGCCGACTCCGAGCCCTGAGCCCT 60

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RESULT 14
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AC ADE50405;
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DT 29-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1430.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003069179-A1.
XX
PD 10-APR-2003.
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PF 11-DEC-2001; 2001US-00015393.
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PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2003-708395/67.
XX P-PSDB; ADE50406.
XX Novel secreted and transmembrane PRO polypeptides useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide and as therapeutic agents e.g. vaccines.
XX Claim 2; SEQ ID NO 115; 555pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
XX
Query Match 100.0%; Score 1808; DB 9; Length 1808;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DT 29-JAN-2004 (first entry)
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KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
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PD 15-MAY-2003.
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PF 10-DEC-2001; 2001US-00013430.
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PR 05-JAN-1999; 98WO-US000106.
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PR 15-SEP-1999; 98WO-US021194.
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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 15-MAY-2000; 2000WO-US013705.
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PR 30-MAY-2000; 2000WO-US014941.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
( GETH ) GENENTECH INC.
Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
Williams PM, Wood WI;
WPI; 2003-765493/72.
P-PSDB; ADE20018.
New isolated PRO polypeptide useful for tissue typing, modulating
biological activity of cell, as molecular weight markers in protein
electrophoresis, for treating arthritis and tumors.
Claim 2; SEQ ID NO 115; 555pp; English.
The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1808; DB 9; Length 1808;
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Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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GenCore version 5.1.6
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Title: US-10-015-393A-115

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Scoring table: IDENTITY NUC
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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LOCUS AX697047 1808 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 115 from Patent WO0078961.
ACCESSION AX697047
VERSION AX697047.1 GI:29498030
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Ferrera, N., Stewart, T. A., Williams, P. M., Baker, K. P., Desnoyers, L.,
Eaton, D. L., Gao, W. Q., Fan, J., Botstein, D., Fong, S., Goddard, A.,
Godowski, P. J., Gurney, A. L., Smith, V., Tumas, D., Wood, W. I.,

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AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Sehagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I., and Godowski,P.		Db	361	CGGACCTGACACTTGGCTTCCCTCAAGTCTATCGAGAGTTTGCAGAAAAGATCATTTGAA	420
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AUTHORS	Clark,H.F.		QY	541	ACAAACTTGTCTGGACAGCTGAAGCTCAGCCCTTCGGGATCATCAACTCTCG	600
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		Db	541	ACAAACTTGTCTGGACAGCTGAAGCTCAGCCCTTCGGGATCATCAACTCTCG	600
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RESULT 3
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DEFINITION Sequence 79 from Patent EP1067182.
ACCESSION AX136157
VERSION AX136157.1 GI:14272565
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashi, K.
TITLE Secretory protein or membrane protein
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Helix Research Institute (JP)
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 source

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 Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,
 Ishii, S., Saiko, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,
 Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, T.
 HRI human cDNA sequencing project
 Unpublished
 2 (bases 1 to 1878)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
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 Research Institute (supported by Japan Key Technology Center etc.);
 cDNA library construction; Institute of Medical Science, University
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CDS

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RESULT 6

BC009881

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC009881 2006 bp mRNA linear PRI 12-NOV-2003
Homo sapiens retinol dehydrogenase 13 (all-trans and 9-cis), mRNA
(cDNA clone MGC:16483 IMAGE:3956119), complete cds.

BC009881.2 GI:33872511

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2006)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Sheezy, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,

Sauchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Schnier, A., Schein, J.E., Jones, S.J., and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2006)

AUTHORS TITLE JOURNAL

Strausberg,R.
Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:14602729.
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadansystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

REMARK COMMENT

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 25 Row: K Column: 11
This clone was selected for full length sequencing because it
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Location/Qualifiers

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LOCUS			
DEFINITION			
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AK122764			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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AUTHORS			
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai H., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K. and Isogai T.			
NEDO human cDNA sequencing project			
Unpublished			
2 (bases 1 to 3055)			
Isogai T. and Yamamoto J.			
Direct Submission			
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.			
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ORIGIN			

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LOCUS Sequence 29 from Patent WO0151638.
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VERSION AX195176.1 GI:15385739
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yang, J., Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Reddy, R.,
Ring, H.Z., Hillman, J.L., Yue, H., Azimzai, Y., Yao, M.G., Gandhi, A.R.,
Nguyen, D.B., Tang, Y.T., Lal, P., and Bandman, O.
TITLE Drug metabolizing enzymes
JOURNAL Patent: WO 0151638-A 29 19-JUL-2001;
Incyte Genomics, Inc. (US)
FEATURES
source location/Qualifiers
1..1282
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Query Match 68.1%; Score 1231.4; DB 6; Length 1282;
Best Local Similarity 99.9%; Pred. No 1e-222; 1; Indels 0; Gaps 0;
Matches 1232; Conservative 0; Mismatches 1;
QY 1 GAGTACCCAGCGGGCTGTGTGACGAAAGCTCCGGCCGACATCCGGAGCGCTGACGCT 60
Db 50 GAGTACCCAGCGGGCTGTGTGACGAAAGCTCCGGCCGACATCCGGAGCGCTGACGCT 109
QY 61 GACGCTGTCCCGGGCCGCGCATGACGCGCTACCTGCTGCCGCTGTCCGCGCTGGGACG 120
Db 110 GACGCTGTCCCGGGCCGCGCATGACGCGCTACCTGCTGCCGCTGTCCGCGCTGGGACG 169
QY 121 GTAGAGGCGCGCGCTGTGTCTCAAGGACTATGTACCGTGGGCTTGGCCGAGCAG 180
Db 170 GTAGAGGCGCGCGCTGTGTCTCAAGGACTATGTACCGTGGGCTTGGCCGAGCAG 229
QY 181 GCCACCATCTCCCTGGGAAGACGCTCATCTGTGAGGGCGCCCAACACAGGACATCGGGAAGCAG 240
Db 230 GCCACCATCTCCCTGGGAAGACGCTCATCTGTGAGGGCGCCCAACACAGGACATCGGGAAGCAG 289
QY 241 ACCGCTTGGAACTGGCCAGGAGGAGGACATCATCTGCTGCCGCTGCCGAGACATGAG 300
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QY 301 AAGTGTGAGCGCGCAGCAAGAGCAGTCCGGGGAGACCTCAATCAACATGTCACGCC 360
Db 350 AAGTGTGAGCGCGCAGCAAGAGCAGTCCGGGGAGACCTCAATCAACATGTCACGCC 409
QY 361 CGGCACTTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTCGAGCAAGAGTCAATGAA 420
Db 410 CGGCACTTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTCGAGCAAGAGTCAATGAA 469

QY 421 GAGGAGGAGCGAGTGGACATTTCTAATCAACACGCGGTGTGATGGTGGCCCCACTGG 480
 Db 470 GAGGAGGAGCGAGTGGACATTTCTAATCAACACGCGGTGTGATGGTGGCCCCACTGG 529
 QY 481 ACCACCGAGAGCGGCTTCGAGATGACATTTGGGTTAAACACCTGGTCACTTCTCTTG 540
 Db 530 ACCACCGAGAGCGGCTTCGAGATGACATTTGGGTTAAACACCTGGTCACTTCTCTTG 589
 QY 541 ACAAACTGTCTGGACAGCTGAAAGCTCAGCGCTCAGCGCTTCGCGGATCATCAACCTCTCG 600
 Db 590 ACAAACTGTCTGGACAGCTGAAAGCTCAGCGCTTCGCGGATCATCAACCTCTCG 649
 QY 601 TCCCTGGCCCATGTTGCTGGACATAGATTTTGAAGCTTGAATGCGGAGAGAGAG 660
 Db 650 TCCCTGGCCCATGTTGCTGGACATAGATTTTGAAGCTTGAATGCGGAGAGAGAG 709
 QY 661 TATAACACCAAGCGGCTACTGCCAGAGCAAGCTCGCATCGTCTCTTCAACCAAGAG 720
 Db 710 TATAACACCAAGCGGCTACTGCCAGAGCAAGCTCGCATCGTCTCTTCAACCAAGAG 769
 QY 721 CTGAGCGCGGCTGCAAGCTCTGTGTGACATGCTCAAGCGCTGACCGCGGCTGGCC 780
 Db 770 CTGAGCGCGGCTGCAAGCTCTGTGTGACATGCTCAAGCGCTGACCGCGGCTGGCC 829
 QY 781 AGGACAGAGCTGGGCGACACACGCGCATCTTCCAGCACTTCTCCAGCACTCACTC 840
 Db 830 AGGACAGAGCTGGGCGACACACGCGCATCTTCCAGCACTTCTCCAGCACTCACTC 889
 QY 841 GGGCCCATCTTCTGGCTGTGGTCAAGAGCGCGGCTGCGCGCTGCGCGGCTGCACTAC 900
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 QY 1021 GCCCGCTGTGGCTTAGAGGCTCCCTCTGTGAGGAGAGCGCGCTCCCGAGATAACT 1080
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 QY 1081 CTGGAGCAGATTTGAAAGCCAGATGCGCGCTCCAGACCGGAGACAGCTGTCGCGCATGC 1140
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 Db 1190 CCGAGCTTCTGGCACTAGCTGAGCGCGGAGACCGAGACTGGCGGCGCGCATGCCCGC 1249
 QY 1201 AGTAGGTTCTAGGGGCGGTGTGGCGCGAGTG 1233
 Db 1250 AGTAGGTTCTAGGGGCGGTGTGGCGCGAGTG 1282

RESULT 9
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 LOCUS 1699 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 6 from Patent WO014446.
 ACCESSION AX179293
 VERSION AX179293.1 GI:14598963
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Meyers, R.
 TITLE 21612, 21615, 21620, 21676, 33756, novel human alcohol
 dehydrogenases

JOURNAL

FEATURES

source

Patent: WO 014446-A 6 21-JUN-2001;
 Millennium Pharmaceuticals, Inc. (US)
 Location/Qualifiers
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/note="unnamed protein product; 21676 ADH"
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Query Match 65.8%; Score 1189.8; DB 6; Length 1699;
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 Matches 1191; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 577 GTAGCAGGCGCGCGGCTGTCTCAAGGACTATGTCAACCGGTGGGGTGTGCCCGCAGCAAG 636
 QY 181 GGCACATCTCTGGGAGACCGGCTCATCGTACGCGGCGGCGCAACACAGGATCGGGAAGCAG 240
 Db 637 GGCACATCTCTGGGAGACCGGCTCATCGTACGCGGCGGCGCAACACAGGATCGGGAAGCAG 696
 QY 241 ACCGCTTGGAACTGGCCAGGAGAGGAGCAACATCATCTCTGGCGCTCCGAGAGCATGGAG 300
 Db 697 ACCGCTTGGAACTGGCCAGGAGAGGAGCAACATCATCTCTGGCGCTCCGAGAGCATGGAG 756
 QY 301 AGTGTGGGCGGCGAGCAAGGACATCGCGGGGAGACCTCATCATCATCATCATCATCATCAT 360
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 QY 421 GAGGAGGAGCGAGTGGACATTTCTAATCAACACGCGGCTGTGATCGCGTGGCGGCTGG 480
 Db 877 GAGGAGGAGCGAGTGGACATTTCTAATCAACACGCGGCTGTGATCGCGTGGCGGCTGG 936
 QY 481 ACCACCGAGGAGCGCTTCGAGATCGAGTTTGGGCTTAACCACTGGGTCACTTTCTCTTG 540
 Db 937 ACCACCGAGGAGCGCTTCGAGATCGAGTTTGGGCTTAACCACTGGGTCACTTTCTCTTG 996
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 Db 997 ACAAACTGTCTGGAGCAAGCTCAAGCGCTTCAGCGCTTCGCGGATCATCAACCTCTCG 1056
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 QY 661 TATAACACCAAGCGGCTTACTGCCAGAGCAAGCTCGCCCATCGTCTCTTCCACCAAGAG 720
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QY 781 AGGACAGAGCTGGGACACACACGGGCATCCATGCTCCACCTTCTCCAGCACCACTC 840
Db 1237 AGGACAGAGCTGGGACACACACGGGCATCCATGCTCCACCTTCTCCAGCACCACTC 1296
QY 841 GGCCCACTTTTGGTGTGTGTCAGAGCCCGGAGCTGGCCGCGCCAGCCAGCACATAC 900
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QY 901 CTGGCCGCTGGCGAGAACTGGCGGATTTCCGGAAAGTACTTCTGATGGACTCAACAG 960
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QY 961 AAGGCCCGGCCCCCGAGCTGAGGATGAGGAGTGGCCCGGAGCTTTGGGCTGAAAGT 1020
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Db 1537 CTGGAGCAGATTTAAAGCTGAGGATGGCGCTCCAGACCGAGACAGTGTCCGCCATGC 1596
QY 1141 CGCAGCTTCCTGGCACTACCTGAGCGGGAGACCCAGGACTGGCGGCGCCA 1193
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RESULT 10
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LOCUS Homo sapiens chromosome 19 clone RP11-700B5, WORKING DRAFT
DEFINITION SEQUENCE, 12 unordered pieces.
AC019238 GI:9838316
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
REFERENCE 2 (bases 1 to 204340)
Waterston,R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9280808.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0700B05
----- Summary Statistics -----
Sequencing vector: M13, 84%
Chemistry: Dye-terminator ET; 84% of reads
Chemistry: Dye-terminator Big Dye; 16% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199676 bases at least Q40
Consensus quality: 200928 bases at least Q30
Consensus quality: 201749 bases at least Q20
Insert size: 236000; agarose-fp
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Insert size: 204523; sum-of-contigs
Quality coverage: 6.54 in Q20 bases; agarose-fp
Quality coverage: 7.57 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 2752: contig of 2752 bp in length
* 2753 2852: gap of unknown length
* 2853 5901: contig of 3049 bp in length
* 5901 6001: gap of unknown length
* 6002 12965: contig of 6964 bp in length
* 12965 13065: gap of unknown length
* 13065 21018: contig of 7953 bp in length
* 21018 21118: gap of unknown length
* 21119 30399: contig of 9281 bp in length
* 30400 40958: gap of unknown length
* 40958 41058: contig of 10459 bp in length
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* 52180 52280: contig of 11122 bp in length
* 52280 65275: gap of unknown length
* 65275 95161: contig of 29786 bp in length
* 95161 95261: gap of unknown length
* 95261 122538: contig of 27277 bp in length
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ORIGIN

Query Match

53.5% Score 966.4; DB 2; Length 204340;

Best Local Similarity 99.9%; Pred. No. 6.8e-173;
Matches 967; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 94119 GGGCCCATCTTCTGGCTGTCTGCTCAAGAGCCCCCGAGCTGGCCGCCAGCCAGCACATAC 94060

QY 901 CTGGCCGTGGCGAGAACTGCGGATGTTTCGGAAAGTACTTCGATGAGCTCAAAACAG 960
Db 94059 CTGGCCGTGGCGAGAACTGCGGATGTTTCGGAAAGTACTTCGATGAGCTCAAAACAG 94000

QY 961 AAGGCCCGCCCGCCCGAGCTGAGGATGAGGAGTGGCCCGAGAGCTTTGGGCTGAAAGT 1020
Db 93999 AAGGCCCGCCCGCCCGAGCTGAGGATGAGGAGTGGCCCGAGAGCTTTGGGCTGAAAGT 93940

QY 1021 GCGCGCTGGTGGCTTAGAGCTCCCTCTGTAGGAGACGCCCTCCCGAGATAACCT 1080
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ACCESSION AC011476
VERSION AC011476.8 GI:22667569
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 187064)
DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 187064)
DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 187064)
DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Aug 16, 2002 this sequence version replaced gi:15022008.
Draft Sequence Produced by DOE Joint Genome Institute
www.igi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTE: Transposon sequencing failed to verify the number of repeat
copies 67315-69359. Unsure number of repeat copies 67315-69359.
NOTE: Shatter libraries failed to resolve dinucleotide repeat
region 171590-171722. Unsure number of repeat copies
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Best Local Similarity 99.7%; Pred. No. 2.8e-172;
Matches 965; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 901 CTGGCCGTGGCGAGAACTGCGGATGTTTCGGAAAGTACTTCGATGAGCTCAAAACAG 960
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QY 961 AAGGCCCGCCCGCCCGAGCTGAGGATGAGGAGTGGCCCGAGAGCTTTGGGCTGAAAGT 1020
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QY 1021 GCGCGCTGGTGGCTTAGAGGCTCCCTCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGTTC 1080
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Db	1134	AGCCGGAGACCCAGGACTG	1153
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ACCESSION			
AX136638			
VERSION			
AX136638.1 GI:14273042			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.			
TITLE			
Secretory protein or membrane protein			
JOURNAL			
Patent: EP 1067182-A 560 10-JAN-2001;			
Helix Research Institute (JP)			
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Qy	1313	TGATGCTTCCCTGGGAATCTAAACTGGGAATGCCGAGGAGGAAGGGCTCTGTGCAT	1372
Db	496	TGATGCTTCCCTGGGAATCTAAACTGGGAATGCCGAGGAGGAAGGGCTCCACGCAC	437
Qy	1373	TGCAGGCCACGCTCAGGAGAGCAGCGGTCTGTCGGGGAGGGTTCAAAGTGTCTCGTG	1432
Db	436	TGCAGGCCACGTCAGAGCCAGGGTCTGTCGGGAGGGTTCCAAGTGTCTCGTG	378
Qy	1433	AAGAGCATGGCAAGTTGTC-TGACACTTGGTGGAATCTGGGTCCCTGTGGGACCTTGT	1491
Db	377	AAGAGCATGGCAAGTTGTC-TGACACTTGGTGGAATCTGGGTCCCTGTGGGACCTTGT	318
Qy	1492	GCATGCATGTCCTCTCTGAGCCCTGGTTCTTCAGCAGTGAGATGCTCAGAAATACCTGC	1551
Db	317	GCATGCATGTCCTCTCTGAGCCCTGGTTCTTCAGCAGTGAGATGCTCAGAAATACCTGC	258
Qy	1552	TGCTCCCATGATGGTGTGGTACAGCAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG	1611
Db	257	TGCTCCCATGATGGTGTGGTACAGCAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG	198
Qy	1612	GGGTGTTTGTCTGAGGGCTTCTGTGCCAGACCCAGCAGCAGCAGTGAGGTGTGCAT	1671
Db	197	GGGTGTTTGTCTGAGGGCTTCTGTGCCAGACCCAGCAGCAGCAGTGAGGTGTGCAT	138
Qy	1672	CCGAGTTTCAGCTCTGCACGGCATGGAGTGGGAACCCACACGCTGCTGTACGAGCC	1731
Db	137	CCTGAGTTTCAGCTCTGCACGGCATGGAGTGGGAACCCACACGCTGCTGTACGAGCC	78
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LOCUS   BD123878              554 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123878
VERSION   BD123878.1 GI:23218823
KEYWORDS  JP 2002017376-A/387.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS   Oka-T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
           Hayashi,K.
TITLE      Secretory protein or membrane protein
JOURNAL   Patent: JP 2002017376-A 387 22-JAN-2002;
           HELIX RESEARCH INSTITUTE
COMMENT   OS Homo sapiens (human)
           PN JP 2002017376-A/387
           PD 22-JAN-2002
           PF 07-JUL-2000 JP 2000253173
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           PI SUGIYAMA,
           PI KOJI HAYASHI
           PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
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Best Local Similarity 96.9%; Pred. No. 2.3e-84;
Matches 540; Conservative 0; Mismatches 13; Indels 4; Gaps 3;

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Qy      1313 TGATGCTTCCCTCGGAATCTAAACTCGGAATGCCGAGGAGGAAGGGGCTCTGTGCACT 1372
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Qy      1373 TGCAGGCCACGTACGAGAGCCAGCGGTGCTGTGTCGGGGAGGTTCCAAAGGTGCTCCGTG 1432
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Qy      1433 AAGAGCATGGCCAAAGTTGTC--TGACACTGGTGGATTCTTGGGTCCCTGTGGGACCTTGT 1491
Db      377 AAGAGCATGGCCAAAGTTGTCCTTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCTTGT 318

Qy      1492 GCATGCATGNCCTCTCTGAGCCTTGGTTCTTCTCAGCAGTCAGATGCTCAGAAATAACTGC 1551
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QY 1732 TGGGATTCGCTGGGACTCCACCTTCCATCTCATCTCTCAATCTCTAGTCCAAACTCGAGCT 1791
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QY 1792 CTCAAACTTGTCTCAATT 1808
Db 17 CTCAAACTTGTCTCAATT 1

RESULT 15

AX406022
LOCUS AX406022 553 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 437 from Patent WO0222660.
ACCESSION AX406022
VERSION AX406022.1 GI:21439483
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F.,
Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 437 21-MAR-2002;
HYSOQ, INC. (US)
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ORIGIN

Query Match 26.2%; Score 473.8; DB 6; Length 553;
Best Local Similarity 99.6%; Pred. No. 2e-79;
Matches 475; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 68 GAGCGCTGTCCCGCGCCGCGCATGAGCGCTACCTGCTCGCGCTGTGCGCGCTGGCGACG 127
QY 121 GTAGCAGGCGCCCGCTGTGTCTCAAGACTATGTACCGGTGGGGCTTCCCCAGCAG 180
Db 128 GTAGCAGGCGCCCGCTGTGTCTCAAGACTATGTACCGGTGGGGCTTCCCCAGCAG 187
QY 181 GCCACCATCCCTGGGAAGCGGTCTGTCAGCGGGGCCAACACAGGCAATCGGGAAGCAG 240
Db 188 GCCACCATCCCTGGGAAGCGGTCTGTCAGCGGGGCCAACACAGGCAATCGGGAAGCAG 247
QY 241 ACCGCTTGAATCGGCCAGAGAGGAGCAATCATCTCGGCTTCCGAGACATGGAG 300

GenCore version 5.1.6
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
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Listing first 45 summaries

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 - 8: em_htc.*
 - 9: gb_est1.*
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 - 11: gb_htc.*
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 - 26: em_gss_phg.*
 - 27: em_gss_vrl.*
 - 28: gb_gss1.*
 - 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	885.4	49.0	896	13	BU848946
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4	828.6	45.8	935	13	BQ682333

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10	740.4	41.0	933	13	BU190625
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12	726	40.2	2696	11	AK028434
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ALIGNMENTS

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LOCUS
DEFINITION
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CDNA Clone CS0DB006Y021 5-PRIME, mRNA sequence.
ACCESSION
BX393531
VERSION
BX393531.1 GI:30627901
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
AUTHORS
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9526.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB006Y021&cluster=9526.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

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DEFINITION BQ682452 982 bp mRNA linear EST 15-JUL-2002
5', mRNA sequence.
ACCESSION BQ682452
VERSION BQ682452.1 GI:21795131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 982)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L12CM380 row: d column: 04
High quality sequence stop: 717.
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GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 47.0%; Score 849; DB 13; Length 982;
Best Local Similarity 96.9%; Pred. No. 1e-157;
Matches 887; Conservative 0; Mismatches 25; Indels 3; Gaps 2;
QY 4 CTACCCAGCGCGCTGTGTGCAAGACTCCGCGCCGACTCCGAGCCTGACCCCTGAC 63
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QY 724 AGCGGGCGGCTGCAAGGCTCTGGTGTGACTGTCAAGCGCCCTGCAACCGCGGTGGCCAGG 783
DB 721 AGCGGGCGGCTGCAAGGCTCTGGTGTGACTGTCAAGCGCCCTGCAACCGCGGTGGCCAGG 780
QY 784 ACAGAGCTGGGCGAGACACACCGGCAATCCATGGCTCCACTTCTCCAGCACCACACTCGGG 843
DB 781 ACAGAGCTGGGCGAGACACACCGGCAATCCATGGCTCCACTTCTCCAGCACCACACTCGGG 840
QY 844 CCCATCTTCT-GGCTGCTGTC--AAGAGCCCGGAGCTGGCGGCCCGCCAGCAGCACAATAC 900
DB 841 CCAATCTTCTGGGCTGCTGGTGTGCTCAAAAACCCCGAAGCTGGGCGGCCCAACCCAGAAATAC 900
QY 901 CTGGCGGTGGCGGAG 915
DB 901 CTGGCGGTGGCGGAG 915

RESULT 4

BQ682333 935 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_8209240 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6265495
DEFINITION 5', mRNA sequence.

ACCESSION BQ682333

VERSION BQ682333.1 GI:21795012

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 935)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapps-r@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2432 row: 1 column: 08

High quality sequence stop: 657.

Location/Qualifiers

1..935

/organism="Homo sapiens"

/mgi_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6265495"

/lab host="DH10B (phage-resistant)"

/clone lib="NIH MGC 112"

/note="Organ: ekin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

FEATURES

Source

Query Match 45.8%; Score 828.6; DB 13; Length 935;

ORIGIN

BM810961 1063 bp mRNA linear EST 05-MAR-2002

AGENCOURT_6587923 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5473329

5', mRNA sequence.

ACCESSION BM810961

VERSION BM810961.1 GI:19127784

KEYWORDS EST.

SOURCE Homo sapiens (human)

Best Local Similarity 98.5%; Pred. No. 1-le-153;
Matches 857; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY 323 ACATCCGCGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGAGACTTGGCTTCCC 382
DB 1 ACATCCGCGGGAGACCTCAATCACCATGTCAAGGCCCGGCACCTGAGACTTGGCTTCCC 60

QY 383 TCAAGTCTATCCGAGAGTTTGGACAAAGATCATTTGAAGAGAGAGAGAGTGGACATTC 442
DB 61 TCAAGTCTATCCGAGAGTTTGGACAAAGATCATTTGAAGAGAGAGAGAGTGGACATTC 120

QY 443 TAATCAACAACCGGGTGTGATGCGGTGCCCGCCACTGGACCAACGAGACGCGCTTCGAGA 502
DB 121 TAATCAACAACCGGGTGTGATGCGGTGCCCGCCACTGGACCAACGAGACGCGCTTCGAGA 180

QY 503 TCGAGTTGGCGCTTAACCACTGGGTCTCTTCTCTTCAAACTTGTCTGTGACCAAGC 562
DB 181 TCGAGTTGGCGCTTAACCACTGGGTCTCTTCTCTTCAAACTTGTCTGTGACCAAGC 240

QY 563 TGAAGACCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTGTGGGC 622
DB 241 TGAAGACCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTGTGGGC 300

QY 623 ACATAGACTTTGACGACTTGAATCGGAGACGAGGAAGTATAACACCAAGCGCGCTACT 682
DB 301 ACATAGACTTTGACGACTTGAATCGGAGACGAGGAAGTATAACACCAAGCGCGCTACT 360

QY 683 GCAGAGCAAGCTCCGCTCTCTTCAACCAAGAGCTGAGCCGGCGCTTCAAGGCT 742
DB 361 GCAGAGCAAGCTCCGCTCTCTTCAACCAAGAGCTGAGCCGGCGCTTCAAGGCT 420

QY 743 CTGCTGTGACTGTCAACCGCTGCAACCGCGGTGGCCAGGACAGAGCTGGGACACACA 802
DB 421 CTGCTGTGACTGTCAACCGCTGCAACCGCGGTGGCCAGGACAGAGCTGGGACACACA 480

QY 803 CGGCGATCCATGCTCCACCTCTCCAGACACACACTGGGGCCCATCTTCTGGCTGCTGG 862
DB 481 CGGCGATCCATGCTCCACCTCTCCAGACACACACTGGGGCCCATCTTCTGGCTGCTGG 540

QY 863 TCAAGAGCCCGGAGCTGGCCCGCCAGCCAGCAGACATACCTGGCGGTGGCGGAGGAACTGG 922
DB 541 TCAAGAGCCCGGAGCTGGCCCGCCAGCCAGCAGACATACCTGGCGGTGGCGGAGGAACTGG 600

QY 923 CGGATGTTCCGGAAGTACTTGGATGAGTCAACCAAGAGCCCGCCCGGCGCTGG 982
DB 601 CGGATGTTCCGGAAGTACTTGGATGAGTCAACCAAGAGCCCGCCCGGCGCTGG 660

QY 983 AGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTCCCGCCCTGGTGGCTTAGAGG 1042
DB 661 AGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTCCCGCCCTGGTGGCTTAGAGG 720

QY 1043 CTCCTCTGTGGGAGGAGCCCGCTCCAGATTAACCTCTGGAGCAGATTGGAAGCCAG 1102
DB 721 CTCCTCTGTGGGAGGAGCCCGCTCCAGATTAACCTCTGGAGCAGATTGGAAGCCAG 780

QY 1103 GATGGCGCCT-CCAGACCCGAGGACAGCTGTCCGCCATGCCCGAGCTTCTGTCATACC 1161
DB 781 GATGGCGCCT-CCAGACCCGAGGACAGCTGTCCGCCATGCCCGAGCTTCTGTCATACC 840

QY 1162 TGAGCC--GGGAGACCCAGGACTGGCGGC 1189
DB 841 TGAACCGGGAAGACCCAGGACTGGCGGC 870

RESULT 5

BM810961

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1063)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: DCTD/DTP
	cDNA Library Preparation: Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Agencourt Bioscience Corporation
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
	Plate: LLCMI984 row: m column: 10
	High quality sequence stop: 602.
FEATURES	Location/Qualifiers
source	1..1063 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5473329" /tissue_type="amelanotic melanoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC 41" /notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN	
Query Match	44.2%; Score 799; DB 12; Length 1063;
Best Local Similarity	95.6%; Pred. No. 9.7e-148;
Matches 853; Conservative	0; Mismatches 36; Indels 3; Gaps 3;
QY	726 CCGCGCGCTGCAAGGCTCTGGTGTGACTGTCAAGCCCTGTCAACGCCCTGTCAACCCCGGGGTGGCCACAGGAC 785
Db	1 CCGCGCGCTGCAAGGCTCTGGTGTGACTGTCAAGCCCTGTCAACGCCCTGTCAACCCCGGGGTGGCCACAGGAC 60
QY	786 AGAGCTGGGAGACACAGGGGATCCATGGCTCCACCTTCTCCAGACACACATCTGGGCC 845
Db	61 AGAGCTGGGAGACACAGGGGATCCATGGCTCCACCTTCTCCAGACACACATCTGGGCC 120
QY	846 CATCTTCTGGCTGTGGTTCAGAGCCCGGAGCTGGCCGCCCGCCAGCCAGCACATACCTGGC 905
Db	121 CATCTTCTGGCTGTGGTTCAGAGCCCGGAGCTGGCCGCCCGCCAGCCAGCACATACCTGGC 180
QY	906 CGTGGCGAGAACTGGCGGATGTTTCGGAAAGTACTTCGATGGACTCAACAGAGGC 965
Db	181 CGTGGCGAGAACTGGCGGATGTTTCGGAAAGTACTTCGATGGACTCAACAGAGGC 240
QY	966 CCCGGCCCCGAGGTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTGGCCG 1025
Db	241 CCCGGCCCCGAGGTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTGGCCG 300
QY	1026 CTTGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGAGCCCTCTCCAGATAA CTTCTGGA 1085
Db	301 CTTGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGAGCCCTCTCCAGATAA CTTCTGGA 360
QY	1086 GCAGATTTGAAGCCAGGATGCGGCTCTCCAGACCGAGGACAGCTGTCCGCCATGCCGCA 1145
Db	361 GCAGATTTGAAGCCAGGATGCGGCTCTCCAGACCGAGGACAGCTGTCCGCCATGCCGCA 420
QY	1146 GCTTCCTGCATCTACTGAGCCGGAGACCCAGAGCTGGCGGGCGCCATGCCCGCAGTAG 1205
Db	421 GCTTCCTGCATCTACTGAGCCGGAGACCCAGAGCTGGCGGGCGCCATGCCCGCAGTAG 480

ORIGIN

Query Match	43.8%	Score	791.4	DB 12	Length	882
Best Local Similarity	97.5%	Pred. No.	2.6e-146			
Matches	857	Conservative	0	Mismatches	16	Indels
					6	Gaps
					5	
QY	23	GCAGCAAGCTCCGGCGGACTCCGGACGCTGACGCTGACGCTGTCCCGCCGCGCCGCA	82			
DB	2	GCAGCAAGCTCCGGCGGACTCCGGACGCTGACGCTGACGCTGTCCCGCCGCGGCA	61			
QY	83	TGAGCGGCTACTGTGTGCGGCTGTGCGGCTGGGACGGTAGGAGCGCGCGCTGTCTGC	142			
DB	62	TGAGCGGCTACTGTGTGCGGCTGTGCGGCTGGGACGGTAGGAGCGCGCGCTGTCTGC	121			
QY	143	TCAAGGACTATGTCAACGGTGGGCTTGGCCCAAGCAAGCCACCATCCCTGGGAAGACGG	202			
DB	122	TCAAGGACTATGTCAACGGTGGGCTTGGCCCAAGCAAGCCACCATCCCTGGGAAGACGG	181			
QY	203	TCATCGTGAGCGGCGCCAAACACAGCATTCGGGAAGACAGCCGCTTGGAACTGGCCAGGA	262			
DB	182	TCATCGTGAGCGGCGCCAAACACAGCATTCGGGAAGACAGCCGCTTGGAACTGGCCAGGA	241			
QY	263	GAGGAGGCAACATCATCTGTGCGCTCCGAGACATGAGAACTGTAGGCGGCGAGCAAGG	322			
DB	242	GAGGAGGCAACATCATCTGTGCGCTCCGAGACATGAGAACTGTAGGCGGCGAGCAAGG	301			
QY	323	ACATCCGGGGAGACCTCAATCAACATGTCAACGCCCGGCACTTGGACTTGGCTTCCC	382			
DB	302	ACATCCGGGGAGACCTCAATCAACATGTCAACGCCCGGCACTTGGACTTGGCTTCCC	361			
QY	383	TCAGTCTACTCGAGAGTTTCAGCAAGATCATTTGAA-GAGGAGGAGCGAGTGACATT	441			
DB	362	TCAGTCTACTCGAGAGTTTCAGCAAGATCATTTGAA-GAGGAGGAGCGAGTGACATT	421			
QY	442	CTAATCAACAAACCGGGGTGTATCGGTGCCCCCACTGGACACCGAGGACGGCTTCGAG	501			
DB	422	CTAATCAACAAACCGGGGTGTATCGGTGCCCCCACTGGACACCGAGGACGGCTTCGAG	481			
QY	502	ATGCAAGTTGGCGTTAAACCACTGGGTCACTTTCTCTTGACAACTTGTCTGTGACAAAG	561			
DB	482	ATGCAAGTTGGCGTTAAACCACTGGGTCACTTTCTCTTGACAACTTGTCTGTGACAAAG	541			
QY	562	CTGAAGAGCTCAGCCCCCTTCGCGA-TCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG	620			
DB	542	CTGAAGAGCTCAGCCCCCTTCGCGGATTCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG	601			
QY	621	GCACATAGACTTTGACGACTTGAATGGCAGACGAGAGTATAACACCAAGAGCGCCTA	680			
DB	602	GCACATAGACTTTGACGACTTGAATGGCAGACGAGAGTATAACACCAAGAGCGCCTA	561			
QY	681	CTGCCAGAGCAAGCTCGCATCGTCTCTTCAACAAGAGCTGAGCGCGCGC-TGCAAG	739			
DB	662	CTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACAAGAGCTGAGCGCGCGCTTGCAG	721			
QY	740	GCTCTGGTGTGACTGTCAACCGCTTGACCCCGCGCTGGCCAGGACAGAGCTGGGCGAGC	799			
DB	722	GCTCTGGTGTGACTGTCAACCGCTTGACCCCGCGCTGGCCAGGACAGAGCTGGGCGAGC	781			
QY	800	ACAC--GGGCATCTCATGGCTCCACCTTCTCCAGCACG-ACACTCGGGCCCATCTTCTGCG	856			
DB	782	ACACGGGGCATCTCATGGTCCACTTCTCAGGCACCAAAATTCGGGACCACTTCTTCTGCG	841			
QY	857	TGCTGTCTAAGAGCCCGAGCTGGCGGCCACCCAGCA	895			
DB	842	TGCTGTCTCAAGAGCCCGAGTTGACGCCAGCCAGCA	880			

RESIST 7

LOCUS	BM914938	1136 bp	linear	EST 12-MAR-2002
DEFINITION	AGENCOURT 6607565 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5480663			
ACCESSION	BM914938			

VERSION	REFERENCE
KEYWORDS	AUTHORS
SOURCE	TITLE
ORGANISM	JOURNAL
	COMMENT

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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	source
FEATURES	

ORIGIN

Query Match	43.0%	Score 777;	DB 12;	Length 1136;
Best Local Similarity	95.0%;	Pred. No. 2.11e-143;		
Matches 814;	Conservative	0;	Mismatches 40;	Indels 3;
				Gaps 1;

Qy	718	GAGCTGAGCCGGCGGCTGCAAGGCTCTGGTGCTGACTGCTCAACGCCCTGCACCCCGCGCTG	777
Db	16	GACGAGGGCGGCGGCTGCAAGTCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGCTG	75
Qy	778	GCCAGGACAGAGCTGGCGAGACACAGGGGCATCCATGGCTCCACCTTCTCCAGCACCACA	837
Db	76	GCCAGGACAGAGCTGGCGAGACACACGGGCAATCCATGGCTCCACCTTCTCCAGCACCACA	135
Qy	838	CTCGGGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGCGGCCACAGCCAGCACA	897
Db	136	CTCGGGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGCGGCCACAGCCAGCACA	195
Qy	898	TACCTGCGCGTGGCGGAGGAACTGGCGGATGTTTCCGAAAGTACTTCGATGGACTCAAA	957
Db	196	TACCTGCGCGTGGCGGAGGAACTGGCGGATGTTTCCGAAAGTACTTCGATGGACTCAAA	255
Qy	958	CAGAAGCCCGGCCCGCCGAGGCTGAGGATGAGAGGTGGCCCGAGGCTTTGGGCTGAA	1017
Db	256	CAGAAGCCCGGCCCGCCGAGGCTGAGGATGAGAGGTGGCCCGAGGCTTTGGGCTGAA	315
Qy	1018	AGTGCCCGCCTGTGGCTTTAGAGGCTCCCTCTGTGAGGAGCAGGCCCTCCCCAGATAA	1077
Db	316	AGTGCCCGCCTGTGGCTTTAGAGGCTCCCTCTGTGAGGAGCAGGCCCTCCCCAGATAA	375
Qy	1078	CCTCTGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGAGCCGAGGACAGCTGTCGCCCA	1137
Db	376	CCTCTGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGAGCCGAGGACAGCTGTCGCCCA	435

Qy 1138 TGCCCGAGCTTCTCTGCACTACTAGCCGGGAGACCCAGGACTGGCGGCCGCGCATGCC 1197
 Db 436 TGCCCGAGCTTCTCTGCACTACTAGCCGGGAGACCCAGGACTGGCGGCCGCGCATGCC 495
 Qy 1198 CGAGTAGGTTCTAGGGGGGGTGGCTGGCCGAGTGGACTGGGCTCAGGTGAGCACTGC 1257
 Db 496 CGAGTAGGTTCTAGGGGGGGTGGCTGGCCGAGTGGACTGGGCTCAGGTGAGCACTGC 555
 Qy 1258 CCGGGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1317
 Db 556 CCGGGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 615
 Qy 1318 CTTCCCTCGGAACTTAAATCTGGAATGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377
 Db 616 CTTCCCTCGGAACTTAAATCTGGAATGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 675
 Qy 1378 GCCACGTCAGGAGAGCCAGCGGTCCTCTGTCGCGGAGGGTTCCAAAGTGTCTCGTGAAGAG 1437
 Db 676 GCCACGTCAGGAGAGCCAGCGGTCCTCTGTCGCGGAGGGTTCCAAAGTGTCTCGTGAAGAG 735
 Qy 1438 CATGGGCAAGTGTCTGACACTTGGTGGATCTTGGTCCCTGT---GGGACCTTGTGCA 1494
 Db 736 CATGGGCAAGTGTCTGACACTTGGTGGATCTTGGTCCCTGT---GGGACCTTGTGCA 795
 Qy 1495 TGCATGCTCTCTCTGAGCCTTGGTTTCTTTCAGCAGTGTGATGCTCAGAAATTAATGCTGT 1554
 Db 796 TGCATGCTCTCTCTGAGCCTTGGTTTCTTTCAGCAGGAGATGCCAGAAATTAATGCTGT 855
 Qy 1555 CTCCCATGATGTTGTGG 1571
 Db 856 CCCCCCGAAGGGGGG 872

RESULT 8
 BU931992 892 bp mRNA linear EST 18-OCT-2002
 LOCUS AGENCOURT_10485713 NIH_MGC_109 Homo sapiens cDNA clone
 DEFINITION IMAGE:6672291 5', mRNA sequence.

ACCESSION BU931992
 VERSION BU931992.1 GI:24120811
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 892)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM952 row: j column: 03
 High quality sequence stop: 617.
 Location/Qualifiers

1..892
 /organism="Homo sapiens"
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 /clone="IMAGE:6672291"
 /tissue_type="teratocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_109"
 /note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.5%; Score 769; DB 13; Length 892;
 Best Local Similarity 96.2%; Pred. No. 7.1e-142;
 Matches 852; Conservative 0; Mismatches 23; Indels 11; Gaps 6;

Qy 160 GTGGGGGTTTCCCGCAGCAGGCCACCATCCCTGGGAGAGCGTTCATCTGTACCGGGGCC 219
 Db 3 GTGGGGGTTTCCCGCAGCAGGCCACCATCCCTGGGAGAGCGTTCATCTGTACCGGGGCC 62
 Qy 220 AACACAGCATCGGAGAGCAGACCGCTTGGAACTGGCAGGAGAGGAGGAGGAGGAGGAGGAG 279
 Db 63 AACACAGCATCGGAGAGCAGACCGCTTGGAACTGGCAGGAGAGGAGGAGGAGGAGGAGGAG 122
 Qy 280 CTGGCTCCGAGACATGGAGAGTGTAGGCGGCGAGCAAGAGACATCCGCGGGAGAGC 339
 Db 123 CTGGCTCCGAGACATGGAGAGTGTAGGCGGCGAGCAAGAGACATCCGCGGGAGAGC 182
 Qy 340 CTCAATCAACATGTCAACCGCGGACCTGTGAGCTTGGCTTCCCTCAAGTCTATCCGAGAG 399
 Db 183 CTCAATCAACATGTCAACCGCGGACCTGTGAGCTTGGCTTCCCTCAAGTCTATCCGAGAG 242
 Qy 400 TTTGAGCAAAAGATCATTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 459
 Db 243 TTTGAGCAAAAGATCATTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 302
 Qy 460 GTGATGGGTTGCCCGCCACTGTGACACCGAGGAGCGGCTTCGAGATGCGAGTTGGGGTTAAC 519
 Db 303 GTGATGGGTTGCCCGCCACTGTGACACCGAGGAGCGGCTTCGAGATGCGAGTTGGGGTTAAC 362
 Qy 520 CACCTGGGTTCACTTCTCTGACAACTTGTGCTGGACAGCTGAAAGCTCAGCCCT 579
 Db 363 CACCTGGGTTCACTTCTCTGACAACTTGTGCTGGACAGCTGAAAGCTCAGCCCT 422
 Qy 580 TGGGGATCATCAACCTCTCTGCTGGCCCATGTTGCTGGGCAATAGACTTTGAGCAG 639
 Db 423 TGGGGATCATCAACCTCTCTGCTGGCCCATGTTGCTGGGCAATAGACTTTGAGCAG 482
 Qy 640 TTGAACTGGCAGAGGAGGAGTATAACCAACCAAGCGGCTTCTCCAGAGCAAGCTCGCC 699
 Db 483 TTGAACTGGCAGAGGAGGAGTATAACCAACCAAGCGGCTTCTCCAGAGCAAGCTCGCC 542
 Qy 700 ATCGTCTCTTCCACCAAGGAGCTGAGCGCGGCTGCAAGGCTCTGCTGTGACTGTCAAC 759
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 Qy 880 GCGCCCGAGCCAGCAGCATCTGCGCC---GTGGCGGAGGAGTGGCGGAGTGTTC-CCGG 935
 Db 723 GCGCCCGAGCCAGCAGCATCTGCGCC---GTGGCGGAGGAGTGGCGGAGTGTTC-CCGG 782
 Qy 936 AAGGTACTTT-CGATGGACTCAAAACAG-AAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 991
 Db 783 AAGGTACTTTGGATGGAGTCAAAACAGAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 842
 Qy 992 AGGTGGCGCGGAGG---CTTTGGGCTGAAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1034
 Db 843 AGGTGGCGCGGAGGCTCTTGGGCGTGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 888

RESULT 9
 BU168826

LOCUS BUI68826 892 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT_8102166 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6252922
 5', mRNA sequence.
 ACCESSION BUI68826
 VERSION BUI68826.1 GI:22682810
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 892)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2399 row: p column: 11
 High quality sequence stop: 641.
 Location/Qualifiers
 1..892
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6252922"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN
 Query Match 41.4%; Score 749.2; DB 13; Length 892;
 Best Local Similarity 95.7%; Pred. No. 6e-138;
 Matches 815; Conservative 0; Mismatches 28; Indels 9; Gaps 4;
 QY 4 CTACCCAGCGCGCTGGTGTGACGAAGCTCCGCGCGGACTCCGGACGCTGACGCGCTGAC 63
 DB 1 CTACCCAGCGCGCTGGTGTGACGAAGCTCCGCGCGGACTCCGGACGCTGACGCGCTGAC 60
 QY 64 GCCTGTCCCGCGCGCGGATGAGCGCTACCTGTGCGGCTGTGCGGCTGGGACCGGTA 123
 DB 61 GCCTGTCCCGCGCGCGGATGAGCGCTACCTGTGCGGCTGTGCGGCTGGGACCGGTA 120
 QY 124 GCAGCGCGCGCGCTGCTCAAGGACTATGTCACGGTGGGCTTGCCCGCAGAGGCC 183
 DB 121 GCAGCGCGCGCGCTGCTCAAGGACTATGTCACGGTGGGCTTGCCCGCAGAGGCC 180
 QY 184 ACCATCCCTGGGAAGACGGTATCTGTGACGGGCGGCAACACAGGATCGGGAAGCAGACC 243
 DB 181 ACCATCCCTGGGAAGACGGTATCTGTGACGGGCGGCAACACAGGATCGGGAAGCAGACC 240
 QY 244 GCCTTGGAACTGGCCAGAGAGGAGGCAACATCATCTGCGCTCCGAGATGAGAG 303
 DB 241 GCCTTGGAACTGGCCAGAGAGGAGGCAACATCATCTGCGCTCCGAGATGAGAG 300
 QY 304 TGTGAGCGCGCAGCAAAAGACATCCGCGGGAGACCTTCAATCACCATGTCAACGCCCGG 363
 DB 301 TGTGAGCGCGCAGCAAAAGACATCCGCGGGAGACCTTCAATCACCATGTCAACGCCCGG 360
 QY 364 CACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTGCGAAGATCATTTGAGAG 423

DB 361 CACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTGCGAAGATCATTTGAAGAG 420
 QY 424 GAGGAGCGAGTGGACATTTCTAATCAACAACGCGGCTGTGATCGGCTGCCCCACTGGACC 483
 DB 421 GAGGAGCGAGTGGACATTTCTAATCAACAACGCGGCTGTGATCGGCTGCCCCACTGGACC 480
 QY 484 ACCGAGGACGGCTTCGAGATGCGAGTTTGGCGTTTAAACCACTGGGTCACCTTCTTTGACA 543
 DB 481 ACCGAGGACGGCTTCGAGATGCGAGTTTGGCGTTTAAACCACTGGGTCACCTTCTTTGACA 540
 QY 544 AACTTGTCTGCTGCAACAAGCTGAAGCCCTCAGCCCTTCGCGATCATCAACCTCTCGTCC 603
 DB 541 AACTTGTCTGCTGCAACAAGCTGAAGCCCTCAGCCCTTCGCGATCATCAACCTCTCGTCC 600
 QY 604 CTGGCCCATGTTGCTGGGCAATAGACTTTGACGACTTTGAACTGGCAGCAGGAGATAT 663
 DB 601 CTGGCCCATGTTGCTGGGCAATAGACTTTGACGACTTTGAACTGGCAGCAGGAGATAT 660
 QY 664 AACACCAAGCGCCCTACTGCCAGAGCAAGCTCGCATCTCCTCTTCCACCAAGAGAGTG 723
 DB 661 AACACCAAGCGCCCTACTGCCAGAGCAAGCTCGCATCTCCTCTTCCACCAAGAGAGTG 720
 QY 724 AGCGCGCGCTGCAA--GGCTCTGTGTGACTGTCAACGCCCTGCAACCC--GGCGTGGC 779
 DB 721 AGCGCGCGCTGCAAAGGGCTCTGTGTGGGACTGTCAACGCCCTGGAACCCCGCGCTGGGCG 780
 QY 780 CAGGACAGAGCTGGG--CAGACACACGCGGATCCATGGCT--CCACCTTCTCCAGCACC 834
 DB 781 CAGGACAAACCTTGGGCAAAACACGGGCGATCTCTTGGCTTCCCTCTTCCAGCAAC 840
 QY 835 ACACCTGGGCGCC 846
 DB 841 ACACCTGGGCGCC 852

RESULT 10
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 DEFINITION 5', mRNA sequence.
 ACCESSION BUI90625
 VERSION BUI90625.1 GI:22704609
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 933)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2359 row: c column: 18
 High quality sequence stop: 656.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6110921"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 41.0%; Score 740.4; DB 13; Length 933;
Best Local Similarity 97.7%; Pred. No. 3.4e-136;
Matches 762; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

QY 4 CTACCCAGGCGGTGTGTGTCAGCAAGCTCCGGCCGACTCCGGAGCCTGACGCTGAC 63
DB 1 CTACCCAGGCGGTGTGTGTCAGCAAGCTCCGGCCGACTCCGGAGCCTGACGCTGAC 60

QY 64 GCCTGTCCCGCGCCCGCATAGCCGCTACCTGTCTGCTCCGCTGTCCGCTGTCCGCTG 123
DB 61 GCCTGTCCCGCGCCCGCATAGCCGCTACCTGTCTGCTCCGCTGTCCGCTGTCCGCTG 120

QY 124 GCAGGCGCGCGTGTCTGCTCAGGACTATGTCACCGTGGGGCTTGCCTCCAGCAAGGCC 183
DB 121 GCAGGCGCGCGTGTCTGCTCAGGACTATGTCACCGTGGGGCTTGCCTCCAGCAAGGCC 180

QY 184 ACCATCCCTGGGAAGCGGTCTATCGTGACGGCGCCCAACACAGGCAATCGGGAAGCAGACC 243
DB 181 ACCATCCCTGGGAAGCGGTCTATCGTGACGGCGCCCAACACAGGCAATCGGGAAGCAGACC 240

QY 244 GCCTTGAAGTCCGAGGAGAGGAGCAATCATCTGCGCTGCGGACATGAGAG 303
DB 241 GCCTTGAAGTCCGAGGAGAGGAGCAATCATCTGCGCTGCGGACATGAGAG 300

QY 304 TGTGAGGCGGCACAAAGAGCATCCGCGGGAGACCTCAATCACCATGTCACGCGCCGG 363
DB 301 TGTGAGGCGGCACAAAGAGCATCCGCGGGAGACCTCAATCACCATGTCACGCGCCGG 360

QY 364 CACTGGAGTGTGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAAGAG 423
DB 361 CACTGGAGTGTGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAAGAG 420

QY 424 GAGGAGCGAGTGACATCTTAATCAACAGCGGGGTGTATGGGTGCGCCCACTGGACC 483
DB 421 GAGGAGCGAGTGACATCTTAATCAACAGCGGGGTGTATGGGTGCGCCCACTGGACC 480

QY 484 ACCGAGGACGGTTCGAGATGCAAGTTTGGCGTTAACCACTGGGTCACTTTCTTTGACA 543
DB 481 ACCGAGGACGGTTCGAGATGCAAGTTTGGCGTTAACCACTGGGTCACTTTCTTTGACA 540

QY 544 AACTTGTGTGACAGCTGAAGCTCAGCCCTTCCGGGATCATCAACCTCTGCTCC 603
DB 541 AACTTGTGTGACAGCTGAAGCTCAGCCCTTCCGGGATCATCAACCTCTGCTCC 600

QY 604 CTGGCCCATCTTGTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAGTAT 663
DB 601 CTGGCCCATCTTGTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAGTAT 660

QY 664 AACACCAAGCCGCTTACTGCCAGAGCAAGCTCGCCATGCTCTTCTTACCAAGGAGCTG 723
DB 661 AACACCAAGCCGCTTACTGCCAGAGCAAGCTCGCCATGCTCTTCTTACCAAGGAGTGT 720

QY 724 AGCGGCGGTGCAAA--GGCTCTGTGTGACTGTCAACGCGCTTGCACCCCGCGGTGCGCA 781
DB 721 AGCGGCGGTGCAAAAGGCTCTGTGTGACTGTCAACGCTTGCACCCCGCGGTGCGCA 780

RESULT 11
Bill17371
LOCUS 602867919F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:5016556 5',
DEFINITION mRNA sequence.
ACCESSION Bill17371
VERSION Bill17371.1 GI:14568272

KEYWORDS

Source Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1019)
NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LICM1827 row: e column: 05
High quality sequence stop: 755.

FEATURES

Location/Qualifiers

1..1019

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:5016556"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 40.3%; Score 727.8; DB 12; Length 1019;
Best Local Similarity 92.7%; Pred. No. 1.1e-133;
Matches 895; Conservative 0; Mismatches 57; Indels 13; Gaps 12;

QY 735 GCAGGCTCTGTGCTGACTGTCTCAAC--CCCTGCACCCCGCGTGGCCAGACAGAGCTGG 793
DB 2 GCAGGCTCTGTGCTGACTGTCAACGGCCCTGTCAACCCCGCGTGGCCAGACAGAGCTGG 61

QY 794 GCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACACACACTCGGCGCCATCTTCT 853
DB 62 GCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACACACACTCGGCGCCATCTTCT 121

QY 854 GCCTGTGCTGTCAGAGCCCGAGCTGCGCCAGCCAGCCAGCAGACATAGCTGGCGTGGCGG 913
DB 122 GCCTGTGCTGTCAGAGCCCGAGCTGCGCCAGCCAGCCAGCAGACATAGCTGGCGTGGCGG 181

QY 914 AGGAAGTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAAACAGAGCCCGCGGCC 973
DB 182 AGGAAGTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAAACAGAGCCCGCGGCC 241

QY 974 CCAGGCTGAGAGTGAAGAGGTGCGCGAGGCTTTGGGCTGAAAGTGCAGGCTGGTGG 1033
DB 242 CCAGGCTGAGAGTGAAGAGGTGCGCGAGGCTTTGGGCTGAAAGTGCAGGCTGGTGG 300

QY 1034 GCTTAGAGCTCCCTCTGTGAGGAGCAGCCCTTCCCGAGATACCTCTTGAGGAGAGATTT 1093
DB 301 GCTTAGAGCTCCCTCTGTGAGGAGCAGCCCTTCCCGAGATACCTCTTGAGGAGAGATTT 360

QY 1094 GAAAGCCAGGATGGCGCTTCCAGACCCAGGAGACAGCTGTCCGCCATGCCCGAGCTTCTG 1153
DB 361 GAAAGCCAGGATGGCGCTTCCAGACCCAGGAGACAGCTGTCCGCCATGCCCGAGCTTCTG 420

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polyA_site 2696
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ORIGIN
Query Match 40.2%; Score 726; DB 11; Length 2696;
Best Local Similarity 82.2%; Pred. No. 4e-133;
Matches 850; Conservative 0; Mismatches 175; Indels 9; Gaps 1;

Qy 62 ACAGCTGTCCTCCCGCGGATGAGCGGCTACCTGTCGCGCTGTCGGCGCTGGGACGG 121
Db 120 ACCCTTTTCCCAAGCTGGATGAGCGGCTTTCTGTCGCGGTCCGTAGTGGGACGG 179
Qy 122 TAGCAGCGCGCGCTGCTCTCAAGACATATGTCACCGTGGGGCTTCCCGCAGCAAG 181
Db 180 TGATCGCGCGCACCGTCTCTCAAGACATATGTCGCTGGTGGGGCTTCTCCAGCAAG 239
Qy 182 CCACCATCTCTGGAAAGACGCTCATCTGTGACGGGCGCCAAACAGCAGCATCGGAAGCA 241
Db 240 CCACCATCTCTGGAAAGACGCTTATCTGTGACAGGAGCCAAACAGCAGCATCGGAAGCA 299
Qy 242 CCAGCTTGGAACTGGCGAGAGAGGAGGCAACATCATCTGGGCTCCCGAGCATGGAGA 301
Db 300 CTGCTTTGGAGCTGGCTTAAAGAGGAGGCAACCTCATCTGGGCTCTGTGATGGAGA 359
Qy 302 AGTGTGAGCGCGAGCAAGGACATCGCGGGAGACCTCTCAATCAACATGTCAGCGCC 361
Db 360 AGTGTGAGCGCGAGTAGACATCTGTGTCAACAGCAGCGGTGATCGCGTGCCACACTGA 419
Qy 362 GGACCTTGGACTTGGCTTCCCTCAAGTCTATCCGAGGTTTGCAGCAAGATCATTTGAAG 421
Db 420 AACGCTTAGACTTGGCTTCCCTCAAGTCTATCCGAGGTTTGCAGCAAGATCATTTAAG 479
Qy 422 AGGAGGAGCGAGTGGACATTTCAATCAACAGCGGGTGTGATCGGTGCGCCCACTGGA 481
Db 480 AGGAGGAGCGAGTAGACATTTCTGTGTCAACAGCAGCGGTGATCGGTGCGCCACACTGA 539
Qy 482 CCACGAGGAGCGGCTTCAGATGACGTTTGGCGTTTACACCTTGGTGCATCTTCTTGA 541
Db 540 CCATGAGGATGGCTTTGAGATGACGTTTGGTGTCAACTACTTGGGCGCATTTTCTATTGA 599
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Db 780 TGAGCCCGGCTGCAAGGCTCTGGTGTGACTGTCAAGCGCTTGCAACCCCGTGGCCA 839
Qy 782 GGACAGAGCTGGGAGACACACGGGATCCATGCTCCACTTCTCCAGCAGCAGCAGCTCG 841
Db 840 GGACAGAGCTGGGAGACATACGGGATCCATGCTCCACTTCTCCAGCAGCAGCAGCTCG 899
Qy 842 GGCCCATCTTCTGGCTGTGCTCAAGAGCCCGAGCTGGCGCGCCAGCCAGCAGCATACC 901
Db 900 GGCCCTTCTTCTGGCTGTGCTCAAGAGTCCCGAGCTGGCGCGCCAGCCAGCAGCATATC 959
Qy 902 TGGCGGTGGGAGAACTGGGAGATGTTTCCGGAAGTACTTGCATGGGCTCAACAGA 961
Db 960 TGGCGGTGGGAGAACTGGGAGATGTTTCCGGAAGTACTTGCATGGGCTCAACAGA 1019
Qy 962 AGGCCCCCGGCGGCTGAGGATGAGGAGGTGGCGCGGAGGCTTTGGGCTGAAAGTG 1021
Db 1020 AGGCTCCATCTCTGAGGCTGAAGATGAGGAAGTAGCCCGCAGACTTTGGAGCGAAGTG 1079

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Qy 1022 CCGCCTGGTGGGCTTAG-----AGGCTCCCTGTGTGAGGAGCAGCCCTCCCCA 1072
Db 1080 CCGCTTTGGTGGGCTTGGCCATGCTCATGATCCCTCGGAGAGGACATGCCATTCCA 1139
Qy 1073 GATAACCTCTGGAG 1086
Db 1140 GATAACCTTCAGAG 1153

RESULT 13
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601346972F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687808 5',
mRNA sequence.
ACCESSION BE559808
VERSION BE559808.1 GI:9803527
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 756)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM379 row: P column: 17
High quality sequence stop: 753.
Location/Qualifiers
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/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

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Query Match 40.0%; Score 724; DB 10; Length 756;
Best Local Similarity 99.1%; Pred. No. 5.5e-13;
Matches 749; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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Qy 61 GAGCGCTGTCCCGCGCGGATGAGCGCTTACCTGTCTGCGCTGTGCGCGTGGGACG 120
Db 61 GAGCGCTGTCCCGCGCGGATGAGCGCTTACCTGTCTGCGCTGTGCGCGTGGGACG 120
Qy 121 GTAGCAGGCGCGCGCTGTCTCAAGGACTATGTCAACGGTGGGGCTTGCCTCAGCAAG 180
Db 121 GTAGCAGGCGCGCGCTGTCTCAAGGACTATGTCAACGGTGGGGCTTGCCTCAGCAAG 180
Qy 181 GCCACCATCTCTGGGAAGACGCTCATCTGTGACGGGCGGCAACAGGATCGGGAGCAG 240

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Db 181 GCCACCATCCTGGGAAGACGGTCATCGTGAGCGGCGCCACACAGGATCGGGAAGCAG 240
Qy 241 ACCGCTTTGGAACCTGGCCAGAGAGGAGGCAACATCATCTCTGGCTCCGAGACATGGAG 300
Db 241 ACCGCTTTGGAACCTGGCCAGAGAGGAGGCAACATCATCTCTGGCTCCGAGACATGGAG 300
Qy 301 AAGTGTGAGGCGGCGAGCAAAAGGACATCGCGGGGAGACCTTCATCAACCATGTCAACGCC 360
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Db 361 CGGCACCTTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTTCAGCAAAAGATCAATTGAA 420
Qy 421 GAGGAGGAGCGAGTGGACATCTTATCAACACCGGGTGATGCGGTGCGCCCATCTGG 480
Db 421 GAGGAGGAGCGAGTGGACATCTTATCAACACCGGGTGATGCGGTGCGCCCATCTGG 480
Qy 481 ACCACCGAGGCGGCTTCGAGATGAGTTTGGCGTTAACCACTGGGTCACTTTCTC-TT 539
Db 481 ACCACCGAGGCGGCTTCGAGATGAGTTTGGCGTTAACCACTGGGTCACTTTCTCTTT 540
Qy 540 GACAACTTGTCTGGACAGCTGAAGACCTCAGCCCTTCGCGGATCATCAACCTCTC 599
Db 541 GACAACTTGTCTGGACAGCTGAAGACCTCAGCCCTTCGCGGATCATCAACCTCTC 600
Qy 600 GTCCCTGGCCCATGTGTGCTGGGACATAGACTTTGACGACTTGAATGGCAGAGGAA 659
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Qy 660 GTATTAACCAAGCGGCTACTGCGAGAGAGTCCGATCGCTCTTCCACCAAGGA 719
Db 661 GTATTAACCAAGCGGCTACTGTCAGAGAAGCTCGCCATCGTCTCTTCCACCAAGGA 720
Qy 720 GCTGAGCGCGGCTGCAAGGCTCTGGTGACTGT 755
Db 721 GTTGAGCGCGCGG-TGCAAGGCTCTGGTGACTGT 755

RESULT 14
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DEFINITION UI-B-EJ0-a10-b-02-0-UI.r1 UI-B-EJ0 Homo sapiens cDNA clone
ACCESSION BM723409
VERSION 1
KEYWORDS 734 bp mRNA linear EST 01-MAR-2002
SOURCE UI-B-EJ0-a10-b-02-0-UI 5', mRNA sequence.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 734)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
PUBMED
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers

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optic nerve, retina, Retina Foveal and Macular, RPE and
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/clone_lib="UI-B-EJ0"
/note="Organ: eye; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-B-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AATGGCGCAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina
foveal and macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
```

ORIGIN

Query Match	40.0%;	Score 722.4;	DB 12;	Length 734;
Best Local Similarity	99.7%;	Pred. No. 1.1e-132;		
Matches 723;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

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Db 61 GCGGTTAAACACCTGGGTCACTTTCTTTGACAACTTCTGCTGACAAAGCTGAAAGCC 120
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Db 181 TTTGACGACTTGAATGCGGAGAGGAGTATACACCAAGCCGCTACTGCCAGAGC 240
Qy 691 AAGCTGCGCATCGTCTCTTTCACCAAGGAGCTGAGCCGCGGTGCAAGGCTCTGTGTG 750
Db 241 AAGCTGCGCATCGTCTCTTTCACCAAGGAGCTGAGCCGCGGTGCAAGGCTCTGTGTG 300
Qy 751 ACTGTCAACGCTTGCACCCCGGTGGCCAGAGAGCTGGGAGACACACGCGGCATC 810
Db 301 ACTGTCAACGCTTGCACCCCGGTGGCCAGAGAGCTGGGAGACACACGCGGCATC 360
Qy 811 CATGGCTCCACCTTCTCCAGCACCATCTCGGCGCCCATCTTCTGGCTGCTGGTCAAGAGC 870
Db 361 CATGGCTCCACCTTCTCCAGCACCATCTCGGCGCCCATCTTCTGGCTGCTGGTCAAGAGC 420
Qy 871 CCGGAGTGGCCCGCCAGCCACATACCTACCTGCGGTGGCGGAGAACTGGCGGATGTT 930
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Qy 931 TCCGGAAGTACTTCGATGAGACTCAACAGAGGCGCCCGCCCGCCGAGGCTGAGGATGAG 990
Db 481 TCCGGAAGTACTTCGATGAGACTCAACAGAGGCGCCCGCCCGCCGAGGCTGAGGATGAG 540
Qy 991 GAGTGTGCCCGGAGGCTTTGGGTGAAAGTGGCCGCTGTGGGCTTAGGGCTCCCTCT 1050
Db 541 GAGTGTGCCCGGAGGCTTTGGGTGAAAGTGGCCGCTGTGGGCTTAGGGCTCCCTCT 600

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QY 1051 GTGAGGAGCAGCCCTCCAGATAAAGCTCTGGAGCAGATTGAAAGCCAGGATGGCG 1110
 Db 601 GTGAGGAGCAGCCCTCCAGATAAAGCTCTGGAGCAGATTGAAAGCCAGGATGGCG 660
 QY 1111 CTCAGACCGAGGACAGCTGTCCTCCAGTCGCGCAGCTTCTGGACATACCTGAGCGGG 1170
 Db 661 CTCAGACCGAGGACAGCTGTCCTCCAGTCGCGCAGCTTCTGGACATACCTGAGCGGG 720
 QY 1171 AGACC 1175
 Db 721 AGACC 725

RESULT 15
 BI827579
 LOCUS 603073545F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165650 5',
 DEFINITION mRNA sequence.
 ACCESSION BI827579
 VERSION BI827579.1 GI:15939116
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL1411 row: i column: 11
 High quality sequence stop: 804.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5165650"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 119"
 /notes="Organ: Brain; Vector: pCMV-SPORT6; Site:1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 39.9%; Score 721; DB 12; Length 831;
 Best Local Similarity 98.1%; Pred. No. 2.2e-132;
 Matches 774; Conservative 0; Mismatches 5; Indels 10; Gaps 4;
 QY 1 GAGCTACCCAGCGGCTGGTGTGTCAGCAGCTCCGCGCGACTCCGAGCGC-----CT 53
 Db 42 GAGCTACCCAGCGGCTGGTGTGTCAGCAGCTCCGCGCGACTCCGAGCGCTGAGCGCT 101
 QY 54 GAGCGCTGACGCGCTGTCCCGCGCGCGCATGAGCGCGCTACCTGCTCCGCGCTGTGGCGCT 113
 Db 102 GAGCGCTGACGCGCTGTCCCGCGCGCGCATGAGCGCGCTACCTGCTCCGCGCTGTGGCGCT 161

QY 114 GGCACGGTAGCAGGCGCGCCGCTGCTCTAAGAGCTATGTCAACGGTGGGGCTTGCCC 173
 Db 162 GGCACGGTAGCAGGCGCGCCGCTGCTCTAAGAGCTATGTCAACGGTGGGGCTTGCCC 221
 QY 174 CAGCAGGCGCACCATCCCTGGGAGACGCTCATCGTGACGGCGCCAAACACAGGCAATCGG 233
 Db 222 CAGCAGGCGCACCATCCCTGGGAGACGCTCATCGTGACGGCGCCAAACACAGGCAATCGG 281
 QY 234 GAAGCAGACCGCTTGGAACTGCGCCAGGAGAGGAGGCAACATCATCTCTGGCTTGGCGAGA 293
 Db 282 GAAGCAGACCGCTTGGAACTGCGCCAGGAGAGGAGGCAACATCATCTCTGGCTTGGCGAGA 341
 QY 294 CATGGAGAGGTGTGAGCGCGCAGCAAGGACATCCCGGGGAGACCTCAATCACCATGT 353
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 QY 414 CATGAGAGGAGGAGGAGTGGACATTTCTAATCAACACGGGGGTGTGATCGGTGCC 473
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 QY 474 CCACTGGACCAACCGAGGAGCGCTTCGAGATGCAAGTTTGGCGTTTAAACACCTGGGTCACTT 533
 Db 522 CCACTGGACCAACCGAGGAGCGCTTCGAGATGCAAGTTTGGCGTTTAAACACCTGGGTCACTT 591
 QY 534 TCTCTTGACAAACTTCTGCTGAGCAAGCTGAAAGCTCAGCCCTTCGGGATCATCAA 593
 Db 582 TCTCTTGACAAACTTCTGCTGAGCAAGCTGAAAGCTCAGCCCTTCGGGATCATCAA 641
 QY 594 CCTCTGTCCTCGCCCATGTTGCTGGGCACATAGAC-TTTGACGACTTGAACCTGGCAGA 652
 Db 642 CCTCTGTCCTCGCCCATGTTGCTGGGCACATAGACTTTTGACGACTTGAACCTGGCAGA 701
 QY 653 CGAGGAAGTATAACACAAAGCGCGCTAC-TGCCAGAGCAAGCTCGGCATCGTCTCTTC 711
 Db 702 CGAGGAAGTATAACACAAAGCGCGCTACTTGGCAGAGCAAGCTCGGCATCGTCTCTTC 761
 QY 712 ACCAA-CGAGCTGAGCGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCC 770
 Db 762 ACCAATGAGCTGAGCGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCC 821
 QY 771 CGGCGTGGC 779
 Db 822 GGGCGTGGC 830

Search completed: June 23, 2004, 12:44:37
 Job time : 4863 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2004, 11:03:04 ; Search time 60 Seconds
(without alignments)
1556.720 Million cell updates/sec

Title: US-10-015-393A-116

Perfect score: 1695

Sequence: 1 MSRYLLPLSALGTGAAVL.....ESARLVGLEAPSVREQLPLR 331

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1695	100.0	331	3 AAY99372	Aay99372 Human PRO
2	1695	100.0	331	4 AAB66121	Aab66121 Protein o
3	1695	100.0	331	4 AAE05174	Aae05174 Human dru
4	1695	100.0	331	6 AAE37278	Aae37278 Human gen
5	1695	100.0	331	6 ABO33614	Abo33614 Novel hum
6	1695	100.0	331	7 ABO44467	Abo44467 Human sec
7	1695	100.0	331	7 ABO33491	Abo33491 Novel hum
8	1695	100.0	331	7 ADC17985	Adc17985 Human PRO
9	1695	100.0	331	7 ADD70631	Add70631 Human sec
10	1695	100.0	331	7 ADD39708	Add39708 Human sec
11	1695	100.0	331	7 ADD70154	Add70154 Human sec
12	1695	100.0	331	7 ADD38275	Add38275 Human sec
13	1695	100.0	331	7 ADD39231	Add39231 Human sec
14	1695	100.0	331	7 ADD38754	Add38754 Human sec
15	1695	100.0	331	7 ADD40185	Add40185 Human sec
16	1695	100.0	331	7 ADE50406	Ade50406 Human sec
17	1695	100.0	331	7 ADE20018	Ade20018 Human sec
18	1695	100.0	331	7 ADE49929	Ade49929 Human sec
19	1695	100.0	331	7 ADE21487	Ade21487 Human sec
20	1691	99.8	331	4 AAB84366	Aab84366 Amino aci
21	1691	99.8	331	5 AAU76222	Aau76222 Human 216
22	1688	99.6	331	4 AAB88356	Aab88356 Human mem
23	1340	79.1	260	4 AAB84365	Aab84365 Amino aci
24	1340	79.1	260	5 AAU76221	Aau76221 Human 337
25	1332	78.6	260	4 AAM40387	Aam40387 Human pol

ALIGNMENTS

RESULT 1

ID AAY99372 standard; protein; 331 AA.

XX AAY99372;

XX AC AAY99372;

XX DT 08-AUG-2000 (first entry)

XX DE Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.

XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX OS Homo sapiens.

XX PN WO200012708-A2.

XX PD 09-MAR-2000. ✓

XX PF 01-SEP-1999; 99WO-US020111.

XX PR 01-SEP-1998; 98US-0098715P.

XX PR 01-SEP-1998; 98US-0098749P.

XX PR 01-SEP-1998; 98US-0098750P.

XX PR 02-SEP-1998; 98US-0098803P.

XX PR 02-SEP-1998; 98US-0098821P.

XX PR 02-SEP-1998; 98US-0098843P.

XX PR 09-SEP-1998; 98US-009536P.

XX PR 09-SEP-1998; 98US-009598P.

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PR	03-NOV-1998;	98US-0108902P.	XX		
(GETH) GENENTECH INC.			(GETH) GENENTECH INC.		
Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;			Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;		
WPI; 2000-237871/20.			WPI; 2000-237871/20.		
N-PSDB; AAA37054.			N-PSDB; AAA37054.		
New mammalian DNA sequences encoding transmembrane, receptor or secreted			New mammalian DNA sequences encoding transmembrane, receptor or secreted		
PRO polypeptides, useful for screening of potential peptide or small			PRO polypeptides, useful for screening of potential peptide or small		
molecule inhibitors of the relevant receptor/ligand interactions.			molecule inhibitors of the relevant receptor/ligand interactions.		
Claim 12; Fig 66; 773pp; English.			Claim 12; Fig 66; 773pp; English.		
AAA37022 to AAA37144 encode the new isolated human transmembrane,			AAA37022 to AAA37144 encode the new isolated human transmembrane,		
receptor or secreted PRO polypeptides given in AA99340 to AA99462. The			receptor or secreted PRO polypeptides given in AA99340 to AA99462. The		
transmembrane and receptor PRO proteins can be used for screening of			transmembrane and receptor PRO proteins can be used for screening of		
potential peptide or small molecule inhibitors of the relevant			potential peptide or small molecule inhibitors of the relevant		
receptor/ligand interactions. The polypeptides and nucleotide sequences			receptor/ligand interactions. The polypeptides and nucleotide sequences		
encoding then have various industrial applications, including uses as			encoding then have various industrial applications, including uses as		
pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR			pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR		
primers and hybridisation probes used in the isolation of the PRO			primers and hybridisation probes used in the isolation of the PRO		
polypeptides from the present invention			polypeptides from the present invention		
Sequence 331 AA;			Sequence 331 AA;		
Query Match			Query Match		
Best Local Similarity 100.0%; Score 1695; DB 3; Length 331;			Best Local Similarity 100.0%; Score 1695; DB 3; Length 331;		
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60	QY	1	MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60
DB	1	MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60	DB	1	MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60
QY	61	RCGNIILACRDMKECEAAAKOIRGTHLHHNARHLDLASIKSIREFAAKLIEEERVDI 120	QY	61	RCGNIILACRDMKECEAAAKOIRGTHLHHNARHLDLASIKSIREFAAKLIEEERVDI 120
DB	61	RCGNIILACRDMKECEAAAKOIRGTHLHHNARHLDLASIKSIREFAAKLIEEERVDI 120	DB	61	RCGNIILACRDMKECEAAAKOIRGTHLHHNARHLDLASIKSIREFAAKLIEEERVDI 120
QY	121	LINNAGVMRCPHWTTEDEGFMQFVNHGLGHFLTNLLDLDKLKASAPSIINLSLAHVAG 180	QY	121	LINNAGVMRCPHWTTEDEGFMQFVNHGLGHFLTNLLDLDKLKASAPSIINLSLAHVAG 180
DB	121	LINNAGVMRCPHWTTEDEGFMQFVNHGLGHFLTNLLDLDKLKASAPSIINLSLAHVAG 180	DB	121	LINNAGVMRCPHWTTEDEGFMQFVNHGLGHFLTNLLDLDKLKASAPSIINLSLAHVAG 180
QY	181	HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFKELSRRLQGGSGVTVNALHPGVARTELGRH 240	QY	181	HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFKELSRRLQGGSGVTVNALHPGVARTELGRH 240
DB	181	HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFKELSRRLQGGSGVTVNALHPGVARTELGRH 240	DB	181	HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFKELSRRLQGGSGVTVNALHPGVARTELGRH 240
QY	241	TGIHGSTFSSTTLGFIWLLNKSPLAAQPSYTLAVAEELADVSQKYFDGLKQKAPAPEA 300	QY	241	TGIHGSTFSSTTLGFIWLLNKSPLAAQPSYTLAVAEELADVSQKYFDGLKQKAPAPEA 300
DB	241	TGIHGSTFSSTTLGFIWLLNKSPLAAQPSYTLAVAEELADVSQKYFDGLKQKAPAPEA 300	DB	241	TGIHGSTFSSTTLGFIWLLNKSPLAAQPSYTLAVAEELADVSQKYFDGLKQKAPAPEA 300
QY	301	EDEEVARRLWAEASRLVGLAEPSVEEQPLPR 331	QY	301	EDEEVARRLWAEASRLVGLAEPSVEEQPLPR 331

DB 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331
RESULT 2
ID AAB66121 standard; protein; 331 AA.
AC AAB66121;
XX 02-APR-2001 (first entry)
DT Protein of the invention #33.
DE
XX Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX
XX 20-JUL-1999; 99US-0144758P.
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XX 26-JUL-1999; 99US-0145698P.
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XX 01-SEP-1999; 99WO-US020111.
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XX 30-OCT-1999; 99US-0162506P.
XX
XX 30-NOV-1999; 99WO-US028313.
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XX 02-DEC-1999; 99WO-US028551.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 08-JAN-2000; 2000WO-US000219.
XX
XX 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillman KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 1; Fig 66; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of anti-
XX sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents. The nucleic
XX acids may also be used in gene therapy
XX
XX Sequence 331 AA;
Query Match 100.0%; Score 1695; DB 4; Length 331;
Best Local Similarity 100.0%; Pred No. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRYLLPLSLALGTVAGAAVLKDYVTGGACPSKATIPGKTVITGANTGIGKOTALELAR 60
DB 1 MSRYLLPLSLALGTVAGAAVLKDYVTGGACPSKATIPGKTVITGANTGIGKOTALELAR 60
QY 61 RGGNIIACRDMKECEAAKDIRGETLNHVNARHLDLSIKSIRPEPAKIIIEEERVDI 120
DB 61 RGGNIIACRDMKECEAAKDIRGETLNHVNARHLDLSIKSIRPEPAKIIIEEERVDI 120
QY 121 LINNAGVMRCPHWTTEDGFEMQGVNHLGHFLTNLLLDKIKASAPSRRIINLSLAHVAG 180

DB 121 LINNAGVMRCPHWTTEDGFEMQGVNHLGHFLTNLLLDKIKASAPSRRIINLSLAHVAG 180
QY 181 HIDFDDLNWOTRYKNTKAAQCQKLAIVLFTKELSRRLQSGVTVNALHFGVARTELGRH 240
DB 181 HIDFDDLNWOTRYKNTKAAQCQKLAIVLFTKELSRRLQSGVTVNALHFGVARTELGRH 240
QY 241 TGIHGSTFSTTLLGPIFWLLVKSPPELAAQPSSTYLAABELADVSGKYFDGLKOKAPAPEA 300
DB 241 TGIHGSTFSTTLLGPIFWLLVKSPPELAAQPSSTYLAABELADVSGKYFDGLKOKAPAPEA 300
QY 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331
DB 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331
RESULT 3
AAE05174
ID AAE05174 standard; protein; 331 AA.
XX
XX AAE05174;
XX
XX 12-SEP-2001 (first entry)
XX
XX Human drug metabolising enzyme (DME-5) protein.
XX
XX Human; drug metabolising enzyme; DME-5; immunosuppressive; gene therapy;
XX cystostatic; autoimmune disorder; inflammatory disorder; atherosclerosis;
XX osteoporosis; eye disorder; hepatic tumour; Addison's disease; craniom;
XX rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia;
XX developmental disorder; endocrine disorder; Iritis; acromegaly; epilepsy;
XX thyrotoxicosis; pancreatic disorder; diabetes mellitus; obesity; adenoma;
XX gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma;
XX actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma;
XX cell proliferative disorder.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..17
XX Protein /label= Signal_peptide
XX 18..331
XX /note= "Mature drug metabolising enzyme (DME-5) protein"
XX
XX WO200151638-A2.
XX
XX 19-JUL-2001. ✓
XX
XX 12-JAN-2001; 2001WO-US001174.
XX
XX 14-JAN-2000; 2000US-0176139P.
XX 21-JAN-2000; 2000US-0177443P.
XX 28-JAN-2000; 2000US-0178574P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;
XX Ring HZ, Hillman JL, Yue H, Azimzai Y, Yao MG, Gandhi AR;
XX Nguyen DB, Tang YT, Lal P, Bandman O;
XX WPI; 2001-425874/45.
XX
XX N-PSDB; AAD09940.
XX
XX Drug metabolising enzymes and encoding polynucleotides, useful for
XX diagnosing, treating and/or preventing autoimmune, inflammatory, cell
XX proliferative, developmental, endocrine, eye, metabolic, and
XX gastrointestinal disorders.
XX
XX Claim 1; Page 139-140; 133pp; English.
XX
XX The present sequence is human drug metabolising enzyme (DME-5) protein.
XX Human DME and its nucleic acid molecule are useful for the diagnosis,
XX treatment and prevention of disorders associated with increased or

CC decreased expression of DME. Examples of such disorders include,
 CC autoimmune/inflammatory disorder such as acquired immune deficiency
 CC syndrome (AIDS), rheumatoid arthritis, osteoporosis; cell proliferative
 CC disorder such as actinic keratosis, atherosclerosis; developmental
 CC disorder such as epilepsy, anaemia; endocrine disorder such as
 CC acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as
 CC diabetes mellitus; eye disorder such as conjunctivitis, glaucoma, iritis;
 CC metabolic disorder such as Addison's disease, obesity; gastrointestinal
 CC disorder such as anorexia, dysphagia and hepatic tumours including
 CC nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for
 CC creating 'knockin' humanised animals (pigs) or transgenic animals (mice
 CC or rats) to model human disease. DME DNA is also in useful is Gene
 CC therapy. DME and its immunogenic fragments are useful for screening
 CC libraries of compounds in several drug screening assays
 XX
 SQ Sequence 331 AA;

Query Match 100.0%; Score 1695; DB 4; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-165;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGKQTALRLAR 60
 DB 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGKQTALRLAR 60
 QY 61 RGNIIILACRDMKECEAAAKDIRGETLNHNHVNARHLDLASLSKSIREFAAKIIIEEERVDI 120
 DB 61 RGNIIILACRDMKECEAAAKDIRGETLNHNHVNARHLDLASLSKSIREFAAKIIIEEERVDI 120
 QY 121 LINNAGVNRCPHWTTEDGFEMQFGVNHGHLFLLNLLDKLKASAPRIINLSLAHVAG 180
 DB 121 LINNAGVNRCPHWTTEDGFEMQFGVNHGHLFLLNLLDKLKASAPRIINLSLAHVAG 180
 QY 181 HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFTKELSRRLQSGGVTVNALHPGVARTELGRH 240
 DB 181 HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFTKELSRRLQSGGVTVNALHPGVARTELGRH 240
 QY 241 TGIHGTSSTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAPEA 300
 DB 241 TGIHGTSSTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAPEA 300
 QY 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331
 DB 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331

RESULT 4
 AAE37278
 ID AAE37278 standard; protein; 331 AA.
 XX
 AC AAE37278;
 XX

DT 07-AUG-2003 (first entry)
 XX Human gene 7 encoded secreted protein HDMK89, SEQ ID NO:41.
 DE
 XX Human; secreted protein; hyperproliferative disorder; multiple myeloma;
 KW immune disorder; cancer; acquired immune deficiency syndrome; arthritis;
 KW haematopoietic disorder; systemic lupus erythematosus; atherosclerosis;
 KW reproductive system disorder; musculoskeletal disorder; renal disorder;
 KW cardiovascular disorder; neurofibromatosis; Alzheimer's disease; asthma;
 KW neurological disorder; Parkinson's disease; respiratory disorder; AIDS;
 KW emphysema; bronchitis; endocrine disorder; genetic disorder; psoriasis;
 KW inflammation; congestive heart failure; multiple sclerosis; arrhythmia;
 KW hypertension; urolithiasis; amenorrhoea; epididymitis; anaemia; allergy;
 KW gout; hepatitis; digestive disease; diabetes; diabetes; goitre; infection; wound;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..16
 FT /label= Signal_peptide

FT Protein 17. .331
 FT /note= "Mature human secreted protein"
 XX WO2003038038-A2.
 PN 08-MAY-2003.
 XX
 PD 24-OCT-2002; 2002WO-US033985.
 XX
 PF 26-OCT-2001; 2001US-0330629P.
 XX
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Rosen CA, Ruben SM, Birse CE, Komatsoulis GA, Choi GH;
 XX WPI; 2003-430509/40.
 XX N-PSDB; AAD56357.
 DR
 DR New isolated nucleic acid molecule and human secreted proteins, useful
 XX for diagnosing, preventing or treating diseases e.g. cancer,
 XX atherosclerosis, anemia, multiple myeloma, hypertension, infections or
 XX wounds.
 XX
 XX Claim 11; Page 450-451; 469pp; English.
 PS
 XX AAD56351-AAD56374 represent cDNAs corresponding to 16 human secreted
 CC protein genes and AAE37272-AAE37295 represent the proteins they encode.
 CC AAE37296-AAE37299 represent human secreted protein fragments. The genes
 CC and their corresponding proteins are useful in diagnosing, preventing or
 CC treating diseases or conditions such as hyperproliferative disorders
 CC (e.g. cancer), immune/haematopoietic disorders (e.g. anaemia, multiple
 CC myeloma, arthritis, asthma, acquired immune deficiency syndrome (AIDS),
 CC rheumatoid arthritis, inflammation, psoriasis, diabetes, systemic lupus
 CC erythematosus or allergy), reproductive system disorders (e.g. gout or
 CC amenorrhoea or epididymitis), musculoskeletal disorders (e.g. arthritis,
 CC multiple sclerosis), cardiovascular disorders (e.g. atherosclerosis), genetic
 CC disorders (e.g. neurofibromatosis), renal disorders (e.g. urolithiasis),
 CC neurological disorders (e.g. Alzheimer's disease or Parkinson's disease),
 CC respiratory disorders (e.g. emphysema or bronchitis), endocrine disorders
 CC (e.g. goitre or diabetes), digestive diseases (e.g. hepatitis),
 CC infections or wounds. Polynucleotides of the invention may also be used
 CC for chromosome mapping or drug screening. They are also useful in gene
 CC therapy. The present sequence represents a human secreted protein of the
 CC invention.
 XX
 SQ Sequence 331 AA;

Query Match 100.0%; Score 1695; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-165;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGKQTALRLAR 60
 DB 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGKQTALRLAR 60
 QY 61 RGNIIILACRDMKECEAAAKDIRGETLNHNHVNARHLDLASLSKSIREFAAKIIIEEERVDI 120
 DB 61 RGNIIILACRDMKECEAAAKDIRGETLNHNHVNARHLDLASLSKSIREFAAKIIIEEERVDI 120
 QY 121 LINNAGVNRCPHWTTEDGFEMQFGVNHGHLFLLNLLDKLKASAPRIINLSLAHVAG 180
 DB 121 LINNAGVNRCPHWTTEDGFEMQFGVNHGHLFLLNLLDKLKASAPRIINLSLAHVAG 180
 QY 181 HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFTKELSRRLQSGGVTVNALHPGVARTELGRH 240
 DB 181 HIDFDLNLWQTRKYNKTKAAYCOSKLAIVLFTKELSRRLQSGGVTVNALHPGVARTELGRH 240
 QY 241 TGIHGTSSTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAPEA 300
 DB 241 TGIHGTSSTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAPEA 300
 QY 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331

QY	121	LIINAGVMRC	PHWTTT	EDGFEMQF	GVNHLGHFLLNLLDKL	KASAPSIINLSLAHVAG	180
Db	121	LIINAGVMRC	PHWTTT	EDGFEMQF	GVNHLGHFLLNLLDKL	KASAPSIINLSLAHVAG	180
QY	181	HIDFDLNMQ	TKYNTKAA	YCQSKIAI	VLFTKELSRRLQSGSVT	NALHPGVARTELGRH	240
Db	181	HIDFDLNMQ	TKYNTKAA	YCQSKIAI	VLFTKELSRRLQSGSVT	NALHPGVARTELGRH	240
QY	241	TGIHGSTP	STTLGPIFWLLVKS	PELAAQPS	TYLAVAEELADVSGKY	FDGLKOKAPAEA	300
Db	241	TGIHGSTP	STTLGPIFWLLVKS	PELAAQPS	TYLAVAEELADVSGKY	FDGLKOKAPAEA	300
QY	301	EDEEVARRL	WAESARLV	GLEAPSVREO	PLPR	331	
Db	301	EDEEVARRL	WAESARLV	GLEAPSVREO	PLPR	331	
RESULT 6							
ABO44467							
ID	ABO44467 standard; protein; 331 AA.						
XX	AC ABO44467;						
XX	01-OCT-2003 (first entry)						
DT	Human secreted/transmembrane protein PRO1430.						
DE	Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;						
XX	antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;						
KW	adrenal cortical capillary; endothelial cell growth; wound healing;						
KW	stimulated T-lymphocyte proliferation; immune response suppression;						
KW	neonatal heart hypertrophy; cardiac insufficiency disorder;						
KW	vascular endothelial growth factor; inflammation; mononuclear cell;						
KW	esicophil; diabetes; obesity; or hyper-insulinemia; hypo-insulinaemia;						
KW	chondrocyte redifferentiation; bone disorder; cartilage disorder;						
KW	sports injury; arthritis.						
XX	Homo sapiens.						
OS	US2003044841-A1.						
XX	06-MAR-2003.						
XX	06-DEC-2001; 2001US-00006856.						
PR	01-SEP-1998;	98US-0098716P.					
PR	01-SEP-1998;	98US-0098723P.					
PR	01-SEP-1998;	98US-0098749P.					
PR	01-SEP-1998;	98US-0098750P.					
PR	02-SEP-1998;	98US-0098803P.					
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PR	02-SEP-1998;	98US-0098843P.					
PR	09-SEP-1998;	98US-0099536P.					
PR	09-SEP-1998;	98US-0099598P.					
PR	09-SEP-1998;	98US-0099602P.					
PR	10-SEP-1998;	98US-0099741P.					
PR	10-SEP-1998;	98US-0099754P.					
PR	10-SEP-1998;	98US-0099763P.					
PR	10-SEP-1998;	98US-0099752P.					
PR	10-SEP-1998;	98US-0099808P.					
PR	10-SEP-1998;	98US-0099812P.					
PR	10-SEP-1998;	98US-0099815P.					
PR	15-SEP-1998;	98US-0099816P.					
PR	15-SEP-1998;	98US-0100385P.					
PR	15-SEP-1998;	98US-0100386P.					
PR	15-SEP-1998;	98US-0100390P.					
PR	16-SEP-1998;	98US-0100584P.					
PR	16-SEP-1998;	98US-0100627P.					
PR	16-SEP-1998;	98US-0100661P.					
PR	16-SEP-1998;	98US-0100662P.					
PR	16-SEP-1998;	98US-0100664P.					

PR	17-NOV-1998;	98US-0108807P.					
PR	17-NOV-1998;	98US-0108867P.					
PR	17-NOV-1998;	98US-0108925P.					
PR	18-NOV-1998;	98US-0108848P.					
PR	18-NOV-1998;	98US-0108849P.					
PR	18-NOV-1998;	98US-0108850P.					
PR	18-NOV-1998;	98US-0108851P.					
PR	18-NOV-1998;	98US-0108852P.					
PR	18-NOV-1998;	98US-0108858P.					
PR	18-NOV-1998;	98US-0108904P.					
PR	22-DEC-1998;	98US-0113296P.					
PR	30-DEC-1998;	98US-0114223P.					
PR	05-JAN-1999;	99WO-US000106.					
PR	16-APR-1999;	99US-0129674P.					
PR	23-JUN-1999;	99US-0141037P.					
PR	20-JUL-1999;	99US-0144758P.					
PR	26-JUL-1999;	99US-0145698P.					
PR	01-SEP-1999;	99WO-US020111.					
PR	15-SEP-1999;	99WO-US021194.					
PR	29-OCT-1999;	99US-0162506P.					
PR	30-NOV-1999;	99WO-US028313.					
PR	02-DEC-1999;	99WO-US028551.					
PR	16-DEC-1999;	99WO-US030095.					
PR	05-JAN-2000;	2000WO-US000219.					
PR	11-FEB-2000;	2000WO-US000376.					
PR	18-FEB-2000;	2000WO-US003565.					
PR	24-FEB-2000;	2000WO-US004342.					
PR	02-MAR-2000;	2000WO-US005004.					
PR	15-MAR-2000;	2000WO-US005841.					
PR	17-MAY-2000;	2000WO-US006884.					
PR	22-MAY-2000;	2000WO-US013705.					
PR	30-MAY-2000;	2000WO-US014042.					
PR	02-JUN-2000;	2000WO-US014941.					
PR	23-AUG-2000;	2000WO-US015264.					
PR	24-AUG-2000;	2000WO-US023522.					
PR	08-NOV-2000;	2000WO-US023328.					
PR	10-NOV-2000;	2000WO-US030952.					
PR	01-DEC-2000;	2000WO-US030873.					
PR	28-FEB-2001;	2001WO-US032678.					
PR	01-MAR-2001;	2001WO-US006520.					
PR	01-JUN-2001;	2001WO-US006666.					
PR	20-JUN-2001;	2001WO-US017800.					
PR	29-JUN-2001;	2001WO-US019692.					
PR	09-JUL-2001;	2001WO-US021066.					
PR	04-SEP-2001;	2001WO-US021735.					
XX	(GETH) GENENTECH INC.						
XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;						
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;						
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;						
PI	Williams PM, Wood WI;						
XX	WPI; 2003-585293/55.						
DR	N-PSDB; ACD68321.						
XX	Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,						
PT	PRO1787 that modulate glucose or free fatty acid uptake by skeletal						
PT	muscle cells, and are useful for treating diabetes, hyper- or hypo-						
PT	Query Match 100.0%; Score 1695; DB 6; Length 331;						
PT	Best Local Similarity 100.0%; Pred. No. 1e-165;						
PT	Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MSRYLLPLS	ALGTGAGAAVL	KDYVTGACPSKAT	IPGKTVITVTGANTG	IGKQTALFELAR	60
Db	1	MSRYLLPLS	ALGTGAGAAVL	KDYVTGACPSKAT	IPGKTVITVTGANTG	IGKQTALFELAR	60
QY	61	RGNNIILAC	RDMEKCEAAK	DIRGETLNHHV	NARHDLASLKS	IRFPAKIIIEEERVDI	120
Db	61	RGNNIILAC	RDMEKCEAAK	DIRGETLNHHV	NARHDLASLKS	IRFPAKIIIEEERVDI	120

RESULT 6

ABO44467	ID	ABO44467	standard; protein; 331 AA.
XX	AC	ABO44467;	
XX	DT	01-OCT-2003	(first entry)
XX	DE	Human secreted/transmembrane protein PRO1430.	
XX	KW	Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;	
KW		adriatic; anorectic; antiarthritic; angiogenesis; cancer;	
KW		adrenal cortical capillary; endothelial cell growth; wound healing;	
KW		stimulated T-lymphocyte proliferation; immune response suppression;	
KW		neonatal heart hypertrophy; cardiac insufficiency disorder;	
KW		vascular endothelial growth factor; inflammation; mononuclear cell;	
KW		eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;	
KW		chondrocyte redifferentiation; bone disorder; cartilage disorder;	
XX		sports injury; arthritis.	
OS		Homo sapiens.	
PN		US2003044841-A1.	
XX	PD	06-MAR-2003.	
XX	PF	06-DEC-2001; 2001US-00006856.	
XX	PR	01-SEP-1998; 98US-0098716P.	
PR		01-SEP-1998; 98US-0098723P.	
PR		01-SEP-1998; 98US-0098749P.	
PR		01-SEP-1998; 98US-0098750P.	
PR		02-SEP-1998; 98US-0098803P.	
PR		02-SEP-1998; 98US-0098821P.	
PR		02-SEP-1998; 98US-0098843P.	
PR		03-SEP-1998; 98US-0098536P.	
PR		03-SEP-1998; 98US-0098598P.	
PR		03-SEP-1998; 98US-0098598P.	
PR		03-SEP-1998; 98US-0098602P.	
PR		03-SEP-1998; 98US-0098642P.	
PR		10-SEP-1998; 98US-0098741P.	
PR		10-SEP-1998; 98US-0098754P.	
PR		10-SEP-1998; 98US-0098763P.	
PR		10-SEP-1998; 98US-0098792P.	
PR		10-SEP-1998; 98US-0098808P.	
PR		10-SEP-1998; 98US-0098812P.	
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PR		10-SEP-1998; 98US-0098816P.	
PR		15-SEP-1998; 98US-0100385P.	
PR		15-SEP-1998; 98US-0100388P.	
PR		15-SEP-1998; 98US-0100390P.	
PR		16-SEP-1998; 98US-0100584P.	
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PR		16-SEP-1998; 98US-0100661P.	
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PR 17-SEP-1998; 98US-0106683P.
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 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0101014P.
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 PR 22-SEP-1998; 98US-0101279P.
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 PR 29-SEP-1998; 98US-0102207P.
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 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-0103328P.
 PR 07-OCT-1998; 98US-0103339P.
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 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105165P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0106500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.

PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108805P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023532.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Deanovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Fan J, Faoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-492259/46.

DR N-PSDB; ACH04423.
 XX

XX Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating various cardiac insufficiency
 PT disorders, bone and/or cartilage disorders such as sports injuries and
 PT arthritis.

PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0218517.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99WO-US020111.
PR 01-SEP-1999; 99WO-US0201194.
PR 15-SEP-1999; 99US-00403297.
PR 18-OCT-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US030095.
PR 16-DEC-1999; 2000WO-US0002179.
PR 05-JAN-2000; 2000WO-US000376.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-0082636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX (GETH) GENENTECH INC.
XX
XX
PI Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski Fu, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;
XX
XX WPI; 2003-585292/55.
DR N-PSDB; ACD67967.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 12; Fig 66; 561pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I), having at least 80% sequence identity to a sequence
Query Match 100.0%; Score 1695; DB 7; Length 331;
Best Local Similarity 100.0%; Pred. No. le-165; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0;
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DB 1 MSRYLLPLSALGTVAGAAVLLKDVVTGGACPSKATIPGKTVITGANTGKQTALSLAR 60
QY 61 RGNIIILACRDMKCEAAAKDIRGETLNHHVNAHDLASIKSIREFAAKIIEEERVDI 120
DB 61 RGNIIILACRDMKCEAAAKDIRGETLNHHVNAHDLASIKSIREFAAKIIEEERVDI 120
QY 121 LINNAGVMRCPHWTTEDEGFEMQFVNHLCHELLTNLLLDKLKASAPSRRIINLSSLAHVAG 180
DB 121 LINNAGVMRCPHWTTEDEGFEMQFVNHLCHELLTNLLLDKLKASAPSRRIINLSSLAHVAG 180
QY 181 HIDFDLNNQTRKNTKAAKQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240
DB 181 HIDFDLNNQTRKNTKAAKQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240
QY 241 TGIHGSTFSSITLGPFWLLVKSPELAAOPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300
DB 241 TGIHGSTFSSITLGPFWLLVKSPELAAOPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300
QY 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331
DB 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331
RESULT 8
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ID ADCl7985 standard; protein; 331 AA.
XX
XX AC ADCl7985;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human PRO polypeptide #33.
XX
XX KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
XX genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN US2003064925-A1.
XX
XX PD 03-APR-2003.
XX
XX PF 10-DEC-2001; 2001US-00013907.
XX
XX PR 01-SEP-1998; 98US-0098716P.
XX PR 01-SEP-1998; 98US-0098723P.
XX PR 01-SEP-1998; 98US-0098749P.
XX PR 01-SEP-1998; 98US-0098750P.
XX PR 02-SEP-1998; 98US-0098803P.
XX PR 02-SEP-1998; 98US-0098821P.
XX PR 02-SEP-1998; 98US-0098843P.
XX PR 03-SEP-1998; 98US-0098536P.
XX PR 09-SEP-1998; 98US-0099596P.

PR	09-SEP-1998;	98US-0095598P.	PR	22-OCT-1998;	98US-0105266P.
PR	09-SEP-1998;	98US-0095602P.	PR	26-OCT-1998;	98US-0105693P.
PR	09-SEP-1998;	98US-0095642P.	PR	26-OCT-1998;	98US-0105694P.
PR	10-SEP-1998;	98US-0095741P.	PR	27-OCT-1998;	98US-0105807P.
PR	10-SEP-1998;	98US-0095754P.	PR	27-OCT-1998;	98US-0105881P.
PR	10-SEP-1998;	98US-0095763P.	PR	27-OCT-1998;	98US-0105882P.
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PR	10-SEP-1998;	98US-0095808P.	PR	28-OCT-1998;	98US-0106023P.
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PR	10-SEP-1998;	98US-0095815P.	PR	28-OCT-1998;	98US-0106030P.
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PR	15-SEP-1998;	98US-0100388P.	PR	28-OCT-1998;	98US-0106178P.
PR	15-SEP-1998;	98US-0100390P.	PR	29-OCT-1998;	98US-0106248P.
PR	16-SEP-1998;	98US-0100584P.	PR	29-OCT-1998;	98US-0106384P.
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PR	16-SEP-1998;	98US-0100651P.	PR	30-OCT-1998;	98US-0106500P.
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PR	18-SEP-1998;	98US-0100848P.	PR	17-NOV-1998;	98US-0108775P.
PR	18-SEP-1998;	98US-0100849P.	PR	17-NOV-1998;	98US-0108775P.
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PR	18-SEP-1998;	98US-0101068P.	PR	17-NOV-1998;	98US-0108788P.
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PR	22-SEP-1998;	98US-0101279P.	PR	17-NOV-1998;	98US-0108802P.
PR	23-SEP-1998;	98US-0101471P.	PR	17-NOV-1998;	98US-0108805P.
PR	23-SEP-1998;	98US-0101472P.	PR	17-NOV-1998;	98US-0108807P.
PR	23-SEP-1998;	98US-0101474P.	PR	17-NOV-1998;	98US-0108867P.
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PR	23-SEP-1998;	98US-0101477P.	PR	18-NOV-1998;	98US-0108849P.
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PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108855P.
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PR	29-SEP-1998;	98US-0102207P.	PR	30-DEC-1998;	98US-0114223P.
PR	29-SEP-1998;	98US-0102240P.	PR	05-JAN-1999;	99WO-US000106.
PR	29-SEP-1998;	98US-0102307P.	PR	16-APR-1999;	98US-0139674P.
PR	29-SEP-1998;	98US-0102330P.	PR	23-JUN-1999;	98US-0141037P.
PR	29-SEP-1998;	98US-0102331P.	PR	20-JUL-1999;	98US-0144758P.
PR	30-SEP-1998;	98US-0102484P.	PR	26-JUL-1999;	98US-0145698P.
PR	30-SEP-1998;	98US-0102487P.	PR	01-SEP-1999;	99WO-US020111.
PR	30-SEP-1998;	98US-0102570P.	PR	15-SEP-1999;	99WO-US021194.
PR	01-OCT-1998;	98US-0102571P.	PR	29-OCT-1999;	99US-0162506P.
PR	01-OCT-1998;	98US-0102687P.	PR	30-NOV-1999;	99WO-US028313.
PR	02-OCT-1998;	98US-0102965P.	PR	02-DEC-1999;	99WO-US028551.
PR	06-OCT-1998;	98US-0103258P.	PR	16-DEC-1999;	99WO-US030095.
PR	06-OCT-1998;	98US-0103258P.	PR	05-JAN-2000;	2000WO-US000219.
PR	06-OCT-1998;	98US-0103449P.	PR	06-JAN-2000;	2000WO-US000376.
PR	07-OCT-1998;	98US-0103314P.	PR	11-FEB-2000;	2000WO-US003565.
PR	07-OCT-1998;	98US-0103315P.	PR	18-FEB-2000;	2000WO-US004342.
PR	07-OCT-1998;	98US-0103328P.	PR	24-FEB-2000;	2000WO-US005004.
PR	07-OCT-1998;	98US-0103335P.	PR	02-MAR-2000;	2000WO-US005841.
PR	07-OCT-1998;	98US-0103336P.	PR	15-MAR-2000;	2000WO-US006884.
PR	07-OCT-1998;	98US-0103336P.	PR	17-MAY-2000;	2000WO-US013705.
PR	08-OCT-1998;	98US-0103633P.	PR	22-MAY-2000;	2000WO-US014042.
PR	08-OCT-1998;	98US-0103678P.	PR	30-MAY-2000;	2000WO-US014941.
PR	08-OCT-1998;	98US-0103679P.	PR	02-JUN-2000;	2000WO-US015264.
PR	08-OCT-1998;	98US-0103711P.	PR	23-AUG-2000;	2000WO-US023522.
PR	14-OCT-1998;	98US-0104257P.	PR	24-AUG-2000;	2000WO-US023328.
PR	20-OCT-1998;	98US-0104987P.	PR	08-NOV-2000;	2000WO-US030952.
PR	20-OCT-1998;	98US-0105000P.	PR	10-NOV-2000;	2000WO-US030873.
PR	20-OCT-1998;	98US-0105002P.	PR	01-DEC-2000;	2000WO-US032678.
PR	21-OCT-1998;	98US-0105104P.	PR	28-FEB-2001;	2001WO-US006520.
PR	22-OCT-1998;	98US-0105169P.	PR	01-MAR-2001;	2001WO-US006666.
PR			PR	01-JUN-2001;	2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-555602/52.
XX N-PSDB; ADC17984.
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 12; SEQ ID NO 116; 555pp; English.
XX
XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The sequences are useful in the preparation of a
CC medicament for treating a condition responsive to a PRO polypeptide. The
CC polypeptides are useful in a number of functional biological assays, as
CC molecular weight markers for protein electrophoresis and as therapeutic
Query Match 100.0%; Score 1695; DB 7; Length 331;
Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKGTALSLAR 60
Db 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKGTALSLAR 60
Qy 61 RGNIIILACDMKCEAAADIRGETLNHVNARHLDLASKIRFPAKIIIEEERVDI 120
Db 61 RGNIIILACDMKCEAAADIRGETLNHVNARHLDLASKIRFPAKIIIEEERVDI 120
Qy 121 LINNAGVRCPHWTTEDGFEMQGVNHLGHFLTNLLDKLKASAPSRINLSSLAHVAG 180
Db 121 LINNAGVRCPHWTTEDGFEMQGVNHLGHFLTNLLDKLKASAPSRINLSSLAHVAG 180
Qy 181 HIDPDDLNWOTRKNTKAAVCOSKLAIVLFTKLSRRLOSGVTVNALHPGVARTLGRH 240
Db 181 HIDPDDLNWOTRKNTKAAVCOSKLAIVLFTKLSRRLOSGVTVNALHPGVARTLGRH 240
Qy 241 TGIHGSTFSTTLGPFWLLVKSPELAAPSTYLAELADVSGKYFDGLKOKAPAPA 300
Db 241 TGIHGSTFSTTLGPFWLLVKSPELAAPSTYLAELADVSGKYFDGLKOKAPAPA 300
Qy 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331
Db 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331
RESULT 9
ID ADD70631 standard; protein, 331 AA.
XX
AC ADD70631;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1430.
XX
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX

OS Homo sapiens.
XX
XX US2003099625-A1.
XX
XX 29-MAY-2003.
XX
XX 12-DEC-2001; 2001US-00015386.
XX
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 01-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100919P.
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PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
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PR 23-SEP-1998; 98US-0101473P.
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PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
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PR

PR 06-OCT-1998; 98US-0103449P.
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 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105134P.
 PR 22-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 27-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 98US-0114223P.
 PR 16-APR-1999; 98US-0129674P.
 PR 23-JUN-1999; 98US-0141037P.
 PR 20-JUL-1999; 98US-0144758P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 01-SEP-1999; 98US-0145698P.
 PR 15-SEP-1999; 98US-0145698P.
 PR 29-OCT-1999; 98US-0162506P.
 PR 30-NOV-1999; 98US-0162506P.
 PR 02-DEC-1999; 98US-0162506P.
 PR 16-DEC-1999; 98US-0162506P.
 PR 05-JAN-2000; 98US-0162506P.
 PR 06-JAN-2000; 98US-0162506P.

PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 22-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-874602/81.
 DR N-PSDB; ADD70630.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
 PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
 XX
 PS Claim 12; SEQ ID NO 116; 553pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 Query Match 100.0%; Score 1695; DB 7; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-165;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITVGANTGIGKQTALELAR 60
 DB 1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITVGANTGIGKQTALELAR 60
 QY 61 RGNIIILACRDMKCEAAAKDIRGETLNHVNAREHDLASLKSIREFAAKIIEEERVDI 120
 DB 61 RGNIIILACRDMKCEAAAKDIRGETLNHVNAREHDLASLKSIREFAAKIIEEERVDI 120
 QY 121 LINNAGVMRCPHWTTEDEFGFEMQFVGNHGLHFLTNLLDLKASAPSIINLSSLAHVAG 180
 DB 121 LINNAGVMRCPHWTTEDEFGFEMQFVGNHGLHFLTNLLDLKASAPSIINLSSLAHVAG 180
 QY 181 HIDFDDLWQTRKYNKAAVQSKLAI VLFTELKSLRRLOQSGVTVNALHPGVARTELGRH 240
 DB 181 HIDFDDLWQTRKYNKAAVQSKLAI VLFTELKSLRRLOQSGVTVNALHPGVARTELGRH 240
 QY 241 TGIHGSTFSSTLTGIFFWLLVKSPDLAQPSTYLAABELADVSGKYDGLKQKAPAPEA 300
 DB 241 TGIHGSTFSSTLTGIFFWLLVKSPDLAQPSTYLAABELADVSGKYDGLKQKAPAPEA 300
 QY 301 EDEEVARRLWAEARLVGLLEAPSVREQLPR 331
 DB 301 EDEEVARRLWAEARLVGLLEAPSVREQLPR 331
 RESULT 10
 ADD39708
 ID ADD39708 standard; protein; 331 AA.
 XX

AC ADD39708;
 XX
 DT 15-JAN-2004 (first entry)
 DE Human secreted/transmembrane protein PRO1430.
 XX
 KW Human; secreted; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003083462-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 10-DEC-2001; 2001US-00013913.
 XX
 PR 05-JAN-1999; 99WO-US000106.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US000356.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006566.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KU;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watarabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI: 2003-755122/71.
 DR N-FSDS; ADD39707.
 XX
 PT New secreted and transmembrane PRO polypeptides useful for treating
 PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
 PT hypo-insulinemia, sports injuries and arthritis.
 XX
 PS Claim 12; SEQ ID NO 116; 557pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 123 fully defined sequences as
 CC given in the specification (including their extracellular domains either
 CC or without their associated signal peptides. Also include are the
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a

CC host cell comprising the vector, producing PRO, a chimaeric molecule
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
 CC PRO antibody. PRO is useful as molecular weight markers for protein
 CC electrophoresis and also for chromosome identification. PRO is also
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 CC useful for generating transgenic animals or knock-out animals which are
 CC useful in development and screening useful reagents. PRO NA is also
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g. arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1285, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence represents a PRO protein of the invention.

XX Sequence 331 AA;

Query Match 100.0%; Score 1695; DB 7; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-165;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTVAGAAVLKDYVTGGACPSKATIFGKTVITGANTGIGKQTALRLAR 60
 DB 1 MSRYLLPLSALGTVAGAAVLKDYVTGGACPSKATIFGKTVITGANTGIGKQTALRLAR 60
 QY 61 RGNIIILACRDWKECEAAKDIRGETLNHHVNASHLDLASKSIRFEAAKIIIEEERVDI 120
 DB 61 RGNIIILACRDWKECEAAKDIRGETLNHHVNASHLDLASKSIRFEAAKIIIEEERVDI 120
 QY 121 LINNAGVNRCPHWTEDGFEMQFVGNHGHFLNLLDLKAKAPSRINLSSLAHVAG 180
 DB 121 LINNAGVNRCPHWTEDGFEMQFVGNHGHFLNLLDLKAKAPSRINLSSLAHVAG 180
 QY 181 HIDFDLNNQTKYNTKAAVCSQKLAIVLFTKLSRLQSGSVTVNALHPGVANTELGRRH 240
 DB 181 HIDFDLNNQTKYNTKAAVCSQKLAIVLFTKLSRLQSGSVTVNALHPGVANTELGRRH 240
 QY 241 TGIHGSTFSSTTLGPFWLLVKSPELAAPSTYLAVALADVSGKYFDGLKOKAPAPEA 300
 DB 241 TGIHGSTFSSTTLGPFWLLVKSPELAAPSTYLAVALADVSGKYFDGLKOKAPAPEA 300
 QY 301 EDEEVARRLWAESARLVGLEAPSVREOPLPR 331
 DB 301 EDEEVARRLWAESARLVGLEAPSVREOPLPR 331

RESULT 11
 ADD70154

ID ADD70154 standard; protein; 331 AA.

XX AC ADD70154;

XX 15-JAN-2004 (first entry)

XX Human secreted/transmembrane protein PRO1430.

XX Human; secreted; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.


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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00346374.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
XX
XX WPI; 2003-708344/67.
DR N-PSDB; ADD70153.
DR
XX
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
XX Claim 12; SEQ ID NO 116; 549pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1695; DB 7; Length 331;
Best local Similarity 100.0%; Pred. NO. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRYLLPLSALGTGAGAAVLKKYVTGGACPSKATIPGKTVITGANTGIGKOTALELAR 60
Db 1 MSRYLLPLSALGTGAGAAVLKKYVTGGACPSKATIPGKTVITGANTGIGKOTALELAR 60
QY 61 RGGNIIILACRDMKCEAAKDIIRGETLNHHVNARHLDLASLKSIRBFAAKIIEEERVDI 120
Db 61 RGGNIIILACRDMKCEAAKDIIRGETLNHHVNARHLDLASLKSIRBFAAKIIEEERVDI 120
QY 121 LINNAGVMRCPHWTTEGFMQGVNHLGHFLTNLLLDKLKASAPSRINLSSLAHVAG 180
Db 121 LINNAGVMRCPHWTTEGFMQGVNHLGHFLTNLLLDKLKASAPSRINLSSLAHVAG 180
QY 181 HIDFDLNLWQTKNTKAAVCSQSLAIVLFTKELSRLOGSGVTVNALHPGVARTELGRH 240
Db 181 HIDFDLNLWQTKNTKAAVCSQSLAIVLFTKELSRLOGSGVTVNALHPGVARTELGRH 240
QY 241 TGIHGSFSSFTTIGPIFWLLVKSPELAQAQSTYLVAABELADVSGKFDGLKOKAPAPA 300
Db 241 TGIHGSFSSFTTIGPIFWLLVKSPELAQAQSTYLVAABELADVSGKFDGLKOKAPAPA 300
QY 301 EDEEVARRLWAESARLVGLEAPSVREQLPR 331
Db 301 EDEEVARRLWAESARLVGLEAPSVREQLPR 331

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RESULT 12
ADD38275
ID ADD38275 standard; protein; 331 AA.
XX

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AC ADD38275;
XX
DI 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1430.
XX
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
XX US2003096955-A1.
XX
PD 22-MAY-2003.
XX
PF 07-DEC-2001; 2001US-00012755.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
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PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
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PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
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PR 16-SEP-1998; 98US-0100661P.
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PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
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PR 18-SEP-1998; 98US-0101014P.
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PR 23-SEP-1998; 98US-0101479P.
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PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.

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OY 241 TGHGTFSTTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAEA 300
DB 241 TGHGTFSTTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAEA 300
OY 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331
DB 301 EDEEVARRLWAEARLVGLEAPSVREOPLPR 331

RESULT 13
ADD39231
ID ADD39231 standard; protein; 331 AA.
AC ADD39231;
XX
DT 15-JAN-2004 (first entry)
DE Human secreted/transmembrane protein PRO1430.
XX
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003096954-A1.
XX
PD 22-MAY-2003.
XX
XX 07-DEC-2001; 2001US-00011671.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
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PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 21-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
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PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 29-OCT-1998; 98US-0108564P.
PR 03-NOV-1998; 98US-0108566P.
PR 03-NOV-1998; 98US-0108902P.
PR 03-NOV-1998; 98US-0108905P.
PR 03-NOV-1998; 98US-0106919P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.

PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.
XX Claim 12; SEQ ID NO 116; 555pp; English.
PS The invention relates to an isolated PRO polypeptide (secreted or
XX Query Match 100.0%; Score 1695; DB 7; Length 331;
XX Best Local Similarity 100.0%; Pred. No. 1e-165;
CC Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTGAGAAVLKDYVTGACPSKATIPGKTVITGANTGKQTALSLAR 60
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QY 121 LINNAGVMRCPHWTEDEGFQMGVNHGFLFLNLLDKLKASAPSRINLSLAHVAG 180
Db 121 LINNAGVMRCPHWTEDEGFQMGVNHGFLFLNLLDKLKASAPSRINLSLAHVAG 180
QY 181 HIDFDDLNWQKRYKNTKAAVQSKLAIVLFTKELSRRLQSGVTVNALHSGVARTELGRH 240
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QY 241 TGINGSTFSSSTLGIPIFWLLVKSPELAQAQSTYLVAEELADYSGKYFDGLKKAPAPEA 300
Db 241 TGINGSTFSSSTLGIPIFWLLVKSPELAQAQSTYLVAEELADYSGKYFDGLKKAPAPEA 300
QY 301 EDEEVARLWAEARLVGLEAPSVREQLPR 331
Db 301 EDEEVARLWAEARLVGLEAPSVREQLPR 331

RESULT 15
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ID ADD40185 standard; protein; 331 AA.
XX AC ADD40185;
XX DT 15-JAN-2004 (first entry)
XX DE Human secreted/transmembrane protein PRO1430.
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; celiac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalasassaemia.
XX OS Homo sapiens.
XX PN US2003082627-A1.
XX PD 01-MAY-2003.
XX PF 06-DEC-2001; 2001US-00006117.
PR 01-SEP-1998; 98US-0098716P.
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PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
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PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
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PR 10-SEP-1998; 98US-0099763P.
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PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
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PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-010207P.
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PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
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PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.

PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106454P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
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PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030035.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX (GETH) GENENTECH INC.
PA Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S,
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
XX WPI, 2003-755104/71.
DR N-PSDB; ADD40184.
XX
PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.
XX
PS Claim 12; SEQ ID NO 116; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1695; DB 7; Length 331;
Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60
DB 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60
QY 61 RGNIIILACRDMCKECAAADKIRGETLNHNHVNARHLDLASLKSIREFAAKIIEEERVDI 120
DB 61 RGNIIILACRDMCKECAAADKIRGETLNHNHVNARHLDLASLKSIREFAAKIIEEERVDI 120
QY 121 LINNAGVMRCPHWTTEDEGFEMQFGYNHGHGFLITNLLDKLKASAPSIINLSSLAHVAG 180
DB 121 LINNAGVMRCPHWTTEDEGFEMQFGYNHGHGFLITNLLDKLKASAPSIINLSSLAHVAG 180
QY 181 HIDFDDLNWQTRKYNTKAAVCOSKLAIVLFTKELSRRLQSGGVTYNALHPGVARTELGRH 240
DB 181 HIDFDDLNWQTRKYNTKAAVCOSKLAIVLFTKELSRRLQSGGVTYNALHPGVARTELGRH 240
QY 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAPEA 300
DB 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAPSTYLAABELADVSGKYFDGLKQKAPAPEA 300
QY 301 EDEEVARRLWAEASRLVGLGAPSVREQPLPR 331
DB 301 EDEEVARRLWAEASRLVGLGAPSVREQPLPR 331

Search completed: June 23, 2004, 11:07:00
Job time : 64 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2004, 11:03:04 ; Search time 45 Seconds
(without alignments)
2320.812 Million cell updates/sec

Title: US-10-015-393A-116

Perfect score: 1695

Sequence: 1 MSRYLLPLSALGTGAGAAVL.....ESARLVGLEAPSVREQLPLR 331

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1340	79.1	260	4 Q96G88	Q96G88 homo sapien
2	818	48.3	330	5 Q960C7	Q960C7 drosophila
3	812	47.9	325	5 Q8MZG9	Q8MZG9 drosophila
4	810	47.8	330	5 Q9V4Q3	Q9V4Q3 drosophila
5	802.5	47.3	331	5 Q9V4P9	Q9V4P9 drosophila
6	767.5	45.3	300	5 Q9V4Q2	Q9V4Q2 drosophila
7	734.5	43.3	300	11 Q9RLR8	Q9RLR8 mus musculus
8	728.5	43.0	293	11 Q9RLR9	Q9RLR9 mus musculus
9	695.5	41.0	296	5 Q8MKN1	Q8MKN1 drosophila
10	668.5	39.4	406	5 Q9W4Q4	Q9W4Q4 drosophila
11	579.5	34.2	309	13 Q7T348	Q7T348 brachydanio
12	569	33.6	303	16 Q7U2X4	Q7U2X4 mycobacteri
13	566	33.4	303	16 Q53613	Q53613 mycobacteri
14	561	33.1	290	16 Q8EQH7	Q8EQH7 oceanobacil
15	547.5	32.3	321	10 Q9LGI8	Q9LGI8 oryza sativ
16	547	32.3	317	5 Q9VE80	Q9VE80 drosophila

17	534	31.5	311	16	Q7U200	Q7u200 mycobacteri
18	534	31.5	338	16	Q53726	Q53726 mycobacteri
19	531.5	31.4	304	16	Q9ZBM5	Q9ZBM5 mycobacteri
20	530.5	31.3	327	4	Q96BH7	Q96bh7 homo sapien
21	525	31.0	287	5	Q8TQJ5	Q8TQJ5 drosophila
22	523	30.9	310	16	Q9LZC8	Q9LZC8 streptomyce
23	515	30.4	320	10	P81259	P81259 brassica na
24	513.5	30.3	336	16	Q9RR99	Q9rr99 deinococcus
25	513	30.3	406	5	Q8SZ46	Q8sz46 drosophila
26	511	30.1	331	10	Q8RWJ2	Q8rwj2 arabidopsis
27	504.5	29.8	331	11	Q8BMX8	Q8bmx8 mus musculu
28	502	29.6	331	10	Q8LCE7	Q8lce7 arabidopsis
29	497	29.3	321	10	Q8O924	Q8O924 arabidopsis
30	492.5	29.1	322	16	Q8ZD97	Q8zd97 streptomyce
31	487.5	28.8	350	10	Q9LZ48	Q9LZ48 arabidopsis
32	487	28.7	412	13	Q8O3A8	Q8O3a8 brachydanio
33	485.5	28.6	311	16	Q8YW93	Q8yw93 anabaena sp
34	485	28.6	308	16	Q8ZBP5	Q8zbp5 streptomyce
35	485	28.6	323	16	Q9AB36	Q9ab36 caulobacter
36	484	28.6	414	4	Q9NZC7	Q9nzc7 homo sapien
37	481	28.4	414	4	Q9NRF5	Q9nrf5 homo sapien
38	480.5	28.3	320	10	Q8L9T6	Q8L9t6 arabidopsis
39	476	28.1	312	16	Q89V05	Q89v05 bradyrhizob
40	475.5	28.1	317	16	Q53537	Q53537 mycobacteri
41	475.5	28.1	317	16	Q7VEM5	Q7vem5 mycobacteri
42	471	27.8	414	11	Q91WL8	Q91wl8 mus musculu
43	467	27.6	414	11	Q9ULF5	Q9ulf5 mus musculu
44	464	27.4	306	2	Q8GMF3	Q8gmf3 streptomyce
45	461.5	27.2	306	16	Q8XQU5	Q8xqu5 raistonia s

ALIGNMENTS

RESULT 1

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AC Q96G88;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC EMBL: BC009881; AAH09881.1; -;
DR GO: GO:0016491; P:oxidoreductase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR002198; ADH short.
DR Pfam: PF00106; adh short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 260 AA; 28794 MW; 12C82526B01A3174 CRC64;

Query Match 79.1%; Score 1340; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.1e-99;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 MEKCEAAAKDIRGETLNHHVNAHRLDLASLKSIREFAAKIIEEERVDILINNAGVRCRCP 131

Db 1 MEKCEAAAKDIRGETLNHHVNAHRLDLASLKSIREFAAKIIEEERVDILINNAGVRCRCP 60

Qy 132 HWTEDGFQVGNHGHFLNLLDKLKASAPSRINLLSLAHVAGHIDPDDLNQOT 191

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Qy 192 KXNTKAAYCOSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRTGTHGSTFSST 251
Db 121 KXNTKAAYCOSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRTGTHGSTFSST 180
Qy 252 TLGPIFWLLVKSPELAAPQSTYLAFAELADVSGKYFDGLKOKAPAPAEADEEVARLWA 311
Db 181 TLGPIFWLLVKSPELAAPQSTYLAFAELADVSGKYFDGLKOKAPAPAEADEEVARLWA 240
Qy 312 ESARLVGLEAPSVREQLPLR 331
Db 241 ESARLVGLEAPSVREQLPLR 260

RESULT 2
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ID Q960C7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE SD07613D
GN CS2064 OR BCDA:SD07613.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AY052124; AAK93548.1; -.
DR FlyBase; FBgn0033205; CG2064.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 330 AA; 36591 MW; 1D941F466B2554F5 CRC64;

Query Match 48.3%; Score 818; DB 5; Length 330;
Best Local Similarity 53.9%; Pred. No. 4e-57;
Matches 171; Conservative 44; Mismatches 100; Indels 2; Gaps 2;

Qy 5 LLPUSALGTAGAAV-LLKDYVTGGACPSKATIPGKTVITGANTGIGKOTALELARRGG 63
Db 9 LSPIMNPANTGVGYLFKEVMQGGKFTKDTDETKGVFTVGTANTGIGKETALEIARRGG 68
Qy 64 NIIACRDMKCEAAKDIRGETLNHNHVARHLDLASKLSIRBFAKIIIEEERVDILIN 123
Db 69 TVYLACDMRCEAKDKIETNNQNI FSELDLSLDSIRKFDVGFKEKPKLHVLIN 128
Qy 124 NAGVMRCPHWTEDGFEMQFVNHGHLFTNLLDKLKASAPSRINLSLAHVAGHID 183
Db 129 NAGVMRCPKTLTKDGYELQGLGVNHGHLFTNLLDLKNSAPSRIVVWSSLAHARGSN 188
Qy 184 FDDLNMWTRKNTKAAVCOSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRTGI 243
Db 189 VADLN-SEKSVDEGLAVSQSKLANLVLTRELAKLKGSGVTVNALHPGVVDTLEARNWAF 247
Qy 244 HGSTFSSSTLGPFIWLLVKSPELAAPQSTYLAFAELADVSGKYFDGLKOKAPAPAEDE 303
Db 248 FQTNLVKFLKPMIWPLLKTPKSGAQTSTIYAALDPELKNISGLYFSDCKPKVPAPALDD 307
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Qy 304 EVARRLWAESARLVGLE 320
Db 308 KVAKFLWAESKWTGLD 324

RESULT 3
Q8MZG9 PRELIMINARY; PRT; 325 AA.
ID Q8MZG9; Q9V4Q1;
AC Q8MZG9; Q9V4Q1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE LP06328p (CG2070-PA).
GN CG2070
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mouton S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
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DR HSSP: P50162; 1AEL.
DR FlyBase; FBgn0050491; CG30491.
DR FlyBase; FBgn0050495; CG30495.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PRO0080; SDRFAMILY.
DR SEQUENCE 331 AA; 37137 MW; 5981F6D5453BDC4B CRC64;

Query Match 47.3%; Score 802.5; DB 5; Length 331;
Best Local Similarity 52.2%; Pred. No. 6.9e-56;
Matches 164; Conservative 44; Mismatches 105; Indels 1; Gaps 1;

QY 2 SRYLLPLGALGVAGAAVLLKDYVGGACPKATIPGKTVITGANTGIGKQTALARR 61
DB 9 SRTAFWLSFTGTTGLAFVKDLMOGGQFTKXETNETGKRVFVTGANTGIGKTVREIAKR 68
QY 62 GNNIILACRDMKCBAAAKDINGETLNHHVNAHLDLASLSIRFAAKIIEERVDIL 121
DB 69 GGTVMACRLKKCEAREEIVLETKNKYVYCQCDLASQESIRHFVAAFKREQEHLVL 128
QY 122 INNAGVMECPHWTTEDEGMQGVNHLGHFLLTNLLDLKLKASAPSRINLSSLAHVAGH 181
DB 129 INNAGVMECPRLTSDGIELQGVNMGHFLTNLLDLKLKSPSRIVNVSSLAHTEGE 188
QY 182 IDFDLNLWQTRKNTKAAAYCQSKLAIVFTKELSRLOGSGVTVNALHPGVARTELGHT 241
DB 189 INTGDLN-SDKSYDEGKAYSQSKLANVLTRELAKRLEGTVNTANALHPGVVDVTEIRHM 247
QY 242 GIHGFTSFSTLGLPTFWLLVKSPELAOPSTVLAELADVSGYFDGLKQKAPAPAE 301
DB 248 GFNFNFFAGLFVKPLFWFPVKTPRNGAQTSLVALDPELEKVTGQYFSDCKLKEMAPAT 307
QY 302 DEVARRLWAESAR 315
DB 308 DTQAKWLWAVSEK 321

RESULT 6
QYV4Q2 PRELIMINARY; PRT; 300 AA.
AC Q9V4Q2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG2065 protein (RH23455p)
GN CG2065.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.B., Zhang Q., Chen L.X.,
RA Brandon K.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berwan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Q9R1R9;
AC 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE UBE-1b.
OS RDH11 OR ARSDR1 OR UBE-1b.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Testis;
RA Goto M., Eddy E.M.;
RT "Ubiquitously expressing gene.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL; AB030504; BAA82657.1; -.
DR MGD; MGI:102581; Rdh11.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 300 AA; 33240 MW; 7332230DB9057262 CRC64;
Query Match 43.3%; Score 734.5; DB 11; Length 300;
Best Local Similarity 50.2%; Pred. No. 1.6e-50;
Matches 151; Conservative 51; Mismatches 92; Indels 7; Gaps 2;
QY 19 VLLKDYVTGGACPSKATIPGKTVITGANTGIGKOTALELARGNIIACRDMEKCEAA 78
Db 3 LVLRKSGVCTSNVQPGKVAIVTQANTGIGKETAQDLAQRGARVYLACRDVDKGLA 62
QY 79 AKDIRGETLNHVNARHLDLASLSIREFAAKIIEEERVDILINNAGVRCPTHWTEDG 138
Db 63 AREIQAVTGNQSVFVRKLDLADTKSIRAFADFLAEKHLHLINNAGVMVPCYKTDAG 122
QY 139 FEMQGVNHLGHFLLTNLLDKLKASAPSRILNLSLAHVAGHIDFDLWQTKYNTKA 198
Db 123 FEMHGVNHLGHFLLTHLLLEKESAPSRIVNLSLGHILGRHFNHLOGE-KFYSAGL 181
QY 199 AYCOSKLAIVFTKELSRRLQSGVTNNALHPGVARTELGHTGHTGHSSTTLGLPIFW 258
Db 182 AYCHSKLANILFTKELAKRLKSGVTTSVHPGVHSELTRYSSI-----MRWLWQLFF 235
QY 259 LLVKSPELAQPSVTLAVAEELADVSGKYFDGLKQKAPAEAEDEVARRLWASRLVG 318
Db 236 VFIKTPQGAQTSLYCALTEGLESLSGSHFSDCQLAWVSYQGRNEIARRLWDVSCDLLG 295
QY 319 L 319
Db 296 L 296
RESULT 8
Q9R1R9
ID Q9R1R9 PRELIMINARY; PRT; 293 AA.
AC Q9R1R9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE UBE-1a.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Goto M., Eddy E.M.;

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RT "Isolation of ubiquitously expressing mouse genes.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL; AB030503; BAA82656.1; -.
DR MGD; MGI:102581; Rdh11.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 293 AA; 32442 MW; 1C4FFA9770F0E9D0 CRC64;
Query Match 43.0%; Score 728.5; DB 11; Length 293;
Best Local Similarity 50.8%; Pred. No. 4.8e-50;
Matches 150; Conservative 48; Mismatches 90; Indels 7; Gaps 2;
QY 25 VTGGACPSKATIPGKTVITGANTGIGKOTALELARGNIIACRDMEKCEAAKDIRG 84
Db 2 LSSGVCTSNVQPGKVAIVTQANTGIGKETAQDLAQRGARVYLACRDVDKGLAAREIQ 61
QY 85 ETLNHNHVNARHLDLASLSIREFAAKIIEEERVDILINNAGVRCPTHWTEDGFEMQFG 144
Db 62 VTGNSQVFRKLDLADTKSIRAFADFLAEKHLHLINNAGVMVPCYKTDAGFEMHIG 121
QY 145 VNHGHFLLTNLLDKLKASAPSRILNLSLAHVAGHIDFDLWQTKYNTKAAYCOSK 204
Db 122 VNHGHFLLTHLLLEKESAPSRIVNLSLGHILGRHFNHLOGE-KFYSAGLAYCHSK 180
QY 205 LAIVFTKELSRRLQSGVTNNALHPGVARTELGHTGHTGHSSTTLGLPIFWLVKSP 264
Db 181 LANILFTKELAKRLKSGVTTSVHPGVHSELTRYSSI-----MRWLWQLFFVFIKTP 234
QY 265 ELAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEVARRLWASRLVGL 319
Db 235 QEGAQTSLYCALTEGLESLSGSHFSDCQLAWVSYQGRNEIARRLWDVSCDLLGL 289
RESULT 9
Q8MKN1
ID Q8MKN1 PRELIMINARY; PRT; 296 AA.
AC Q8MKN1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DI 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG30495-PA.
GN CG30495 OR CGI7986.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champ M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Arif J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bernos P.V., Berman B.P., Bhandari D., Bhojshak P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.D., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne S.E., Celniker S.E., Brannon R.C., Rogers Y.,
RA Banon J.C., An H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorset V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Gray A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AE003840; AM71103.1; -;
DR FlyBase; FBN0050495; CG30495.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 296 AA; 33041 MW; 3672586954E8EBF CRC64;
Query Match 41.0%; Score 695.5; DB 5; Length 296;
Best Local Similarity 49.1%; Pred. No. 2,1e-47;
Matches 142; Conservative 54; Mismatches 92; Indels 1; Gaps 1;

QY 27. GGACPSKATIPGKTVITGANTGICQTALELAREGGNILLACRDMKECAAKDIRGET 86
DB 3 GGRFRQTDGKVAIVTGGNTGLGTGVTWELARGAIVYACRNKEKVERARRIVKET 82
QY 87 LNHHVNAHLDLASKLSIREFAAKIIEBEERVDILLINAGVNRCPHWTTEDEFGNFGV 146
DB 63 GSNVFSRECDLSLSIRKFAENFKKEQVHLHILINNAGVFWPEHRLTKGFEHGLVN 122
QY 147 HGHFLLTLLLDKLKASPSIILNLSIAHVAGHIDPDDLNNWQTRKNTKAAVCSKLA 206
DB 123 HGHFLLTLLLDKLKASPSIILNLSIAHVAGHIDPDDLNNWQTRKNTKAAVCSKLA 181
QY 207 IVLFTKELSRRLQSGGVTVNALHPGVARTELGRHTGHTGHSSTTLPFIWLLVKSPEL 266
DB 182 NILFTRELAKLEGVTVNALNPGIADTEIARNMIFFTQKFAQIILFLLWAVMKTPOK 241
QY 267 AQPSTYLAVAEELADVSKYFDGLKQKAPAEAEDESVARELWAEASR 315
DB 242 GAQTTLYAALDPLERVSQGYFSDCALAPVAPALDDQQAOWLWAOSEK 290
RESULT 10
Q9W404 PRELIMINARY; PRT; 406 AA.
ID Q9W404
AC Q9W404;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE CG3842 protein.
GN CG3842.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankkocn C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weinstein J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Best Local Similarity 44.2%; Pred. No. 2.9e-37;
Matches 134; Conservative 46; Mismatches 101; Indels 22; Gaps

QY 34 ATTP---GKTVTTCAGTGGKQTALARRGGNIILACRDMKECAAAKDTRGETLNHH 90
DB 7 ADIPDTGRTAVITCANTGLCFETAALAAGAHGVLAENVLDKGQAARITEATPGAE 66
QY 91 VNARHDLASLKSIFEPAAKIIEBEERVDIILNNAQVNRCPHTTTDDGFEMOFQVNHLGH 150
DB 67 VELQELDITSLSAVERAAAQLSKDHQRIDLLINNAGVVYTPROTADGFEMOFGTNHIGH 126
QY 151 FLLTNILLDKLASAPSRRIINSLIAH-VAGHIDFDLLNWOTRYNTKAAYCOSKLAIVL 209
DB 127 FALTGLLIDRLLPVAGSRVWTISSVGHRIRAAIHFDLQWE-RYRVRAVYAQGAKLANUL 185
QY 210 FYKELSRRLOQSGSVTVN-ALHPGVARTELGRHTGIHGSTFTSSTTLGPFIWLLVKSPELAA 268
DB 186 FTVELQRLRAPGGTTIIVASHPGVSNTLE-----VRNNRPFLVAVAAILAPLMQDAELGA 240
QY 269 QSTVYLVAEELADVSGKYF--DGL-----KQKAPAPAEDEEVARRLRWAESARLVGL 319
DB 241 LPT--LRAATDPANVGQYFGPDGFEIGRVPKVVASSAQSHDEQLQRLLRVAVSELTGV 298
QY 320 EAP 322
DB 299 VVP 301

RESULT 13
ID OS3613 PRELIMINARY; PRT; 303 AA.
AC OS3613;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Oxidoreductase (Oxidoreductase, short-chain dehydrogenase/reductase family).
GN RV0068 OR MT0074 OR MTV030.11.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fittwell T., Gentles S., Hamlin N., Holroyd S., Hornsbey T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
RT Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Paterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayan L.J., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A., Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (ISDR) FAMILY.
CC ENBL; AL021428; CAAL6249.1; -.
DR ENBL; AE006919; AAK44298.1; -.
DR PIR; E70848; E70848.

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QY 39 KTVITVGTANTGIGKOTALELARRGNTIILACRDMKECEAAAKDIRGETLNNHVNARHDL 98
Db 4 KTIIVTGTANTGMLATTIELAKGIHVIMACRDTKRGNEAKKAMEESNTNISLYQCCL 63
QY 99 ASLKSIREFAKIIEEERVDILNNAGVMRCPEHTTDEGFEMQFGVNHGHELLTNLL 158
Db 64 GMSIESIKFPADQIKEDFKDGLNNAGVSLKTKTDEGFESMTGVMHGLHLLHLL 123
QY 159 DKLKASAPSRILNLSLAHVAGHIDFDLNNQTRKYNTKAAYCQSKLAIVLFTKELSRRL 218
Db 124 DVLKKSEQARIINVASGAYKAGTLDYNDMFNRSFNVIKGYGQSKLCNLTLELNKHL 183
QY 219 QGSGVTYNALHPGVARTELG--RRTG-----IHGSTPSTTGLPIFWLLVKSPELAAPST 272
Db 184 EGTNVSTFALHPGAVSTSLGVDROTGFGEKVH-----LLRPF-----LTSBEGAETAI 233
QY 273 YLAVALADYSGKYFDGLKOKAPAPAEDEVARRLWAESARLVGLEAPSRE 326
Db 234 YLATEPKIDHLSGRFYFKKLOPTKYKNWNEDEAKLWDWSIKELGWEHKAIEE 287
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RESULT 15

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Q9LGI8 PRELIMINARY; PRT; 321 AA.
AC Q9LGI8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P009G03.18 protein (P0030H07.1 protein).
GN P009G03.18 OR P0030H07.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_taxID=4530;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare (GA3) genomic DNA, chromosome 1, PAC
clone:P009G03."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBSJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare (GA3) genomic DNA, chromosome 1, PAC
clone:P0030H07."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBSJ databases.
CC -! SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AP002522; BAB03618.1; -.
DR EMBL; AP003045; BAB44039.1; -.
DR Gramene; Q9LGI8; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ
SEQUENCE 321 AA; 34841 MW; DE281A6D5B20D0E9 CRC64;
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Query Match 32.3%; Score 547.5; DB 10; Length 321;
Best Local Similarity 42.3%; Pred No. 1.6e-35;
Matches 137; Conservative 51; Mismatches 111; Indels 25; Gaps 8;

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Db 4 LSLITGKAGASGFGSGSTAEQTAGV---DAT--GLTIVTGGASGIGLETSRVFPAMRGA 58
QY 64 NIILACRDMKECEAAKDIRGETLNNHVNARHDLASLSKISREPAKIIIEEERVDILIN 123
Db 59 HVIIAARNTAASVVRKKIIEENPKAHIDVLKDLSSLSKSVRAFADQFNSMNPILIN 118
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QY 124 NAGVMRCPEHTTDEGFEMQFGVNHGHELLTNLLLDKLKASAPS-----RIINLSSLAHV 178
Db 119 NAGVMFCFFGLSEGGVEMQFATNHLGHPELLTNLLLDNNKATAKSTGIEGRIVNLSVAHL 178
QY 179 AGH-----IDPDDLNWQTRKYNTKAAYCQSKLAIVLFTKELSRRL--QSGVTYNALHPGVA 233
Db 179 HTYPRGIEFDKLN-DEKTYDDKMAYGOSKLANILHAKELSRRLKEEGANITINCVPGLI 237
QY 234 RTELGRHTGIHGSIPTSTTGLPIFWLLVKSPELAAPSTYLAVALADYSGKYFDGLKQ 293
Db 238 MTNLNRH-----SFFLMEVLQFATYILWKSVPQGAATTCCYVGLNPQLKGVITGQYFADCNV 292
QY 294 KAPAPAEDEDEVARRLWAESARLV 317
Db 293 EKTSRFARNDALAKQLWEFSEKLI 316
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Search completed: June 23, 2004, 11:07:58
Job time : 48 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:04:52 ; Search time 139 Seconds
(without alignments)
7218.354 Million cell updates/sec

Title: US-10-015-393A-115
Perfect score: 1808
Sequence: 1 gagctaccaggcgctggt.....actctcaaacctgtcattt 1808

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/prodata/2/ina/5B-COMB.seq:*
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5: /cgn2_6/prodata/2/ina/PCTUS-COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	532	29.4	1352	4	US-09-833-381-931
2	297.8	16.5	2494	4	US-09-724-864-6
3	247.8	13.7	2507	4	US-09-439-313-332
4	247.8	13.7	2507	4	US-09-352-616A-332
5	247.8	13.7	2507	4	US-09-332-149A-332
6	247.8	13.7	2507	4	US-09-636-215-332
7	247.8	13.7	2507	4	US-09-685-166A-332
8	247.8	13.7	2507	4	US-09-688-489-332
9	233.2	12.9	1086	3	US-08-464-400-1
10	233.2	12.9	1086	3	US-08-875-273A-1
11	233.2	12.9	1086	4	US-09-123-386-1
12	233.2	12.9	1086	5	PCT-US95-01827A-1
13	219.6	12.1	234	4	US-09-833-381-933
14	168.6	9.3	4403765	3	US-09-103-840A-2
15	168.6	9.2	4411529	3	US-09-103-840A-1
C 16	139.8	7.7	337	4	US-09-439-313-385
C 17	139.8	7.7	337	4	US-09-352-616A-385
C 18	139.8	7.7	337	4	US-09-636-215-385
C 19	139.8	7.7	337	4	US-09-685-166A-385
C 20	139.6	7.7	1376	4	US-09-489-847-66
C 21	138.8	7.7	4403765	3	US-09-103-840A-2
C 22	138.8	7.7	4411529	3	US-09-103-840A-1
C 23	131.2	7.3	1143	4	US-09-252-991A-16283
C 24	131.2	7.3	1383	4	US-09-252-991A-16511
C 25	131.2	7.3	2400	4	US-09-252-991A-15991
C 26	127.2	7.0	1375	4	US-09-489-847-120
C 27	122.4	6.8	2310	4	US-09-620-312D-206

C	28	106	5.9	222	4	US-09-833-381-932	Sequence 932, App
	29	93.8	5.2	1378	3	US-08-580-545B-1	Sequence 1, Appli
	30	93.8	5.2	1378	3	US-09-262-653A-1	Sequence 1, Appli
	31	88	4.9	1197	2	US-08-530-165-6	Sequence 6, Appli
	32	80.2	4.4	864	2	US-08-901-306-1	Sequence 1, Appli
	33	80.2	4.4	864	2	US-09-180-271-1	Sequence 1, Appli
	34	80.2	4.4	1569	3	US-08-901-306-3	Sequence 3, Appli
	35	80.2	4.4	1569	3	US-09-180-271-3	Sequence 3, Appli
	36	78.8	4.4	825	4	US-09-328-352-4087	Sequence 4087, Ap
	37	71	3.9	771	4	US-09-252-991A-13903	Sequence 13903, A
	38	71	3.9	1419	4	US-09-252-991A-13796	Sequence 13796, A
C	39	71	3.9	1995	4	US-09-252-991A-13546	Sequence 13546, A
	40	68.8	3.8	268	4	US-09-313-294A-2451	Sequence 2451, Ap
	41	54.4	3.0	3196	4	US-09-096-982-4	Sequence 4, Appli
	42	54.4	3.0	3196	2	US-08-553-650A-4	Sequence 4, Appli
	43	53	2.9	1138	3	US-08-581-148C-3	Sequence 3, Appli
	44	51	2.8	948	4	US-09-252-991A-9617	Sequence 9617, Ap
	45	51	2.8	3162	4	US-09-252-991A-9569	Sequence 9569, Ap

ALIGNMENTS

RESULT 1
US-09-833-381-931/c
; Sequence 931, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 931
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1352)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-931

Query Match	29.4%	Score 532;	DB 4;	Length 1352;
Best Local Similarity	81.7%	Pred. No. 3.9e-116;		
Mismatches	638;	Conservative	0;	Mismatches 113; Indels 30; Gaps 1;
QY	420	AGAGGAGGAGGAGTGACATTTCTAATCAACACGGGGTGTGATGGGTCGCCCACTG	479	
DB	1300	AGAGGAGGAGGAGTGACATTTCTAATCAACACGGGGTGTGATGGGTCGCCCACTG	1241	
QY	480	GACCACCGAGGACGGCTTCGAGATGCGATTTGGCGTTAAACACCTGGGTCTCTTT	539	
DB	1240	GACCACCGAGGACGGCTTCGAGATGCGATTTGGCGTTAAACACCTGGGTCTCTTT	1181	
QY	540	GACAACTTGTGTGACAACTTGAAGCTCAGCCCTTCGGGATCATCAACCTCTC	599	
DB	1180	GACAACTTGTGTGACAACTTGAAGCTCAGCCCTTCGGGATCATCAACCTCTC	1121	
QY	600	GTCCTTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAATCGGACGAGAA	659	
DB	1120	GTCCTTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAATCGGACGAGAA	1061	
QY	660	GTATTAACCAAGCGGCTTACTGCCAGAGCAAGCTGCCATCGCTCTTCCACCAAGGA	719	
DB	1060	GTATTAACCAAGCGGCTTACTGCCAGAGCAAGCTGCCATCGCTCTTCCACCAAGGA	1001	
QY	720	GCTGAGCGCGGGTGTGCAAGGCTCTGTGTGACTGTCAACGCCCTGCACCCCGCGTGGC	779	

Db 1000 GGTGAGCCGGGGTTTACGGTTCTGGTGTGACTGTCAACGCCCTTCTCTCAGCGCTCG 941
 QY 780 CAGACACAGCTGGGC-----AGACACACGGGCAT 809
 Db 940 GGAGCAGCCAGGGCTGTGGCGGATGAGAAACCGTGTCTCAGAGGAGGACGTG 881
 QY 810 CCATGGCTCCACTTCTCCAGACACACTCGGGCCCATCTTCTGGCTGTGTCTCAAG 869
 Db 880 GTGCTGACGCTGGAGTCAGCTGTACTCAGGGGCCCATCTTCTGGCTGTGTCTCAAG 821
 QY 870 CCCCAGCTGGCCGCCAGCCAGCACATACCTGGCGTGGCGGAGAACTGGCGGATGT 929
 Db 820 CCCCAGCTGGCCGCCAGCCAGCACATACCTGGCGTGGCGGAGAACTGGCGGATGT 761
 QY 930 TTCGGAAAGTACTTCGATGACTCAACAGAGCCCGCCCGCCCGAGGCTGAGGATGA 989
 Db 760 TTCGGAAAGTACTTCGATGACTCAACAGAGCCCGCCCGCCCGAGGCTGAGGATGA 701
 QY 990 GGAGTGGCCCGGAGCTTTGGGCTGAAAGTGCCCGCTGTGGCTTAGAGGCTCCCTC 1049
 Db 700 GGAGTGGCCCGGAGCTTTGGGCTGAAAGTGCCCGCTGTGGGCTTAGAGGCTCCCTC 641
 QY 1050 TGTGAGGAGCAGCCCTCCCGAGATAACCTCTGGAGCAGATTTGAAAGCCAGATGGCG 1109
 Db 640 CTTGGGGGGTACCCCGCCCTGTAAACCTCGGGGCCATTTTAAAGCCCGGTAGTGG 581
 QY 1110 CTTCCAGACCGAGGACAGCTGTCCGCCATGCCCGAGCTTCTCGCACTACTGAGCCGG 1169
 Db 580 CCTCGAGGGGGCCACCGATCCATCCATTCGGCTATTGTGCCACTAACCTGGGTGG 521
 QY 1170 G 1170
 Db 520 G 520

RESULT 2

US-09-724-864-6
 ; Sequence 6, Application US/09724864
 ; Patent No. 6380362
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Murison, James G.
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
 ; FILE REFERENCE: 11000.105001
 ; CURRENT APPLICATION NUMBER: US/09/724,864
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
 ; PRIOR FILING DATE: 1999-12-23
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 2494
 ; TYPE: DNA
 ; ORGANISM: Rat
 US-09-724-864-6

Query Match 16.5%; Score 297.8; DB 4; Length 2494;
 Best Local Similarity 80.1%; Pred. No. 6.8e-61;
 Matches 366; Conservative 0; Mismatches 82; Indels 9; Gaps 1;
 QY 638 ACTTGAATGGCAGACGAGGAAGTATAACACAAAGCCGCTTACTGCGCAGAGCAAGCTCG 697
 Db 1 ACTTGAATGGCAGATATAAAGATATGACACAGCAGCTTACTGCCAGAGCAAGTTGG 60
 QY 698 CCATGCTCTTCTACCAAGAGAGCTAGCCGGGCTCGAAGGCTCTGGTGTGACTGTCA 757
 Db 61 CTGTTGCTCTTCTACCAAGAGAGCTAGTTCGGCGCTGCAAGGCACTGGTGTGACTGTCA 120
 QY 758 AGCCCTGACCCCGCGCTGGCGAGACAGAGCTGGCGAGACACACCGGCATCCATGGCT 817
 Db 121 ATGCGCTGCACCCCTGGCGTGGCGAGGACGAGCTGGGGCGCATACAGGCATGCACACT 180

QY 818 CCACCTTCTCCAGACCAACACATCGGGGCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGC 877
 Db 181 CTGCGCTTCTGCTGCTCATGCTTGGGCCCTTCTTCTGGCTGCTGTTCAAGAGTCCCCAGC 240
 QY 878 TGGCCGCCAGCCAGCCAGCACATACCTGGCCGTGGGGAGGAACTGGCGGATGTTTCCGGAA 937
 Db 241 TGGCCGCCAGCCAGCCAGCACATACCTGGCTGTGGCAGAGGAACTGGAGAGTGTCTCTGGA 300
 QY 938 ACTACTTCGATGACTCAAAACAGAGGCCCGCCCGCCCGAGGCTGAGATGAGGAGTGG 997
 Db 301 AGTACTTTCGATGACTCAGAGAGAGGCTCCATCTCTGAGGCTGAAAGTGAAGAGTAG 360
 QY 998 CCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAG-----AGGCTCCCT 1048
 Db 361 CCGGAGGCTTTGGGCTGAAAGTGCCCGCTTTGGTGGGCTTGACATGCTCATGGTCT 420
 QY 1049 CTGTGAGGAGCAGCCCTCCCGCAGATTAACCTCTGGA 1085
 Db 421 CTGGGAGGAGCATTCCTCCTCCAGATAACCTTCAGA 457
 RESULT 3
 US-09-439-313-332
 ; Sequence 332, Application US/09439313
 ; Patent No. 6329505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yuqi
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 210121.427C9
 ; CURRENT APPLICATION NUMBER: US/09/439,313
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 332
 ; LENGTH: 2507
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-439-313-332
 Query Match 13.7%; Score 247.8; DB 4; Length 2507;
 Best Local Similarity 55.3%; Pred. No. 4.1e-49;
 Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;
 QY 130 GCGCGCTGCTGCTCAAGACTATGTACCGGTGGGGTGGCCCGAGAGCCACCATC 189
 Db 81 GCTGCGCCCAATCAGGAAATGCTGTCCAGTGGGGTGTGTACATCAACTGTTGAGCTT 140
 QY 190 CTTGGAAACCGTCACTGTGAGCGGCGCAACACAGGATCGGAAAGCAGACCGCTTG 249
 Db 141 CTTGGAAAGTGTGTTGTGTACAGAGCTAATACAGGTATCGGAAAGAGACAGCCAA 200
 QY 250 GAACTGCCCGCAGGAGAGGAGCAACATCATCTGGCTCGCAGACATGGAGAGTGTGAG 309
 Db 201 GAGCTGCTCAGAGAGGAGCTCGAGTATATTTAGCTTGGCGGATGTGAAAAGGGGAA 260
 QY 310 GCGGACCAAGAGACATCCGGGAGACCTCAATCACCATGTCAACCCCGGACCTG 369
 Db 261 TTGGTGCCAAAGAGATCCAGACACAGCAGGGAACAGAGTGTGTTGGGGAACCTG 320
 QY 370 GACTTGGCTTCCCTCAAGTCTATCCAGAGTGTTCAGCAAAAGATCAATTGAAGAGGAG 429
 Db 321 GACCTGCTGACTAAGTCTATTCAGGCTTTTGTAGGGCTTTCTTAGCTGAGGAAAG 380

Qy 430 CGAGTGACATCTTAATCAACAAACGCGGTGTGATCGGTGCGCCCACTGGAACACGAG 489
Db 381 CACCTCCACGTTTTGATCAACAATGACAGAGTATGATGTCGGTACTCGAAGACAGCA 440
Qy 490 GACGGCTTCGAGATGCGAGTTTGGCGTTAAACCACTGGGTGACCTTTCTTCTGACAAACTTG 549
Db 441 GATGGCTTTGAGATGCGACATAGAGTCAACCACTTGGGTCACTTCCTTCTTAAACCACTTG 500
Qy 550 CTGCTGACAACTGCGAAGCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCC 609
Db 501 CTGCTAGAGAACTTAAGGAATCAGCCCATCAAGATAGTAATGTCTTCCCTCGCA 560
Qy 610 CATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGAGAGAGAGAGTATTAACCC 669
Db 561 CATCACCTGGGAAGGATCCATTCATTAACCTGACAGGCGCA---GAAATTTCTCAATGCA 617
Qy 670 AAAGCCGCTACTGCGAGCAAGCTCGCCATCGCTCTCTTCAACAGGAGCTGAGCCGG 729
Db 618 GGCCTGGCTACTGTCAGACAGCTAGCCAGTACATCTTTCACCCAGGAACTGGCCCGG 677
Qy 730 CGGTGCAAGGCTCTGGTGTGACTGTCAAGCCCTGCAACCCCGCGTGGCCAGAGACAG 789
Db 678 AGACTAAAGGCTCTGGCGTTACGACGTATTCTGTACACCTGCGCACAGTCCAACTCGAA 737
Qy 790 CTGGGCGACACAGCGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGSCCATC 849
Db 738 CTGGTTCGGCACTCATCTTTATGAGATGATGT-----GGTGGCTT 779
Qy 850 TTCTGGCTGTGTCAGAGCCCGAGCTGGCCCGCCAGCCAGCACATACCTGGCGGTG 909
Db 780 TTCTGCTTTTTCATCAAGACTCTCAGCAGGAGCCAGACAGCCCTGCACTGTGCCTTA 839
Qy 910 GCGAGGAACCTGGCGATGTTTCGGAAGTACTTCGATGACTCAACAGAGAGCCCGG 969
Db 840 ACAGAGGCTTTGAGATTTAAGTGGGAATCATTTAGTACTGTCTATGTGGCATGGGTC 899
Qy 970 GCGCCCGAGGTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTGGCCCGCTG 1029
Db 900 TCTGCCCCAAGCTCGTAATGAGACTATAGCAAGCGGCTGTGGGAGCTCAGTTGTGACCTG 959
Qy 1030 GTGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCCGACATTAACCTCTGAGCAG 1089
Db 960 CTGGGCTTCCCAATAGACTAAAGGAGTGGCCAGTGGACCCAGAGAAAGACTGACGAG 1019
Qy 1090 ATTTGAAAG 1098
Db 1020 ACTACACAG 1028

RESULT 4

US-09-352-616A-332
; Sequence 332, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2507
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-352-616A-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;
Best Local Similarity 55.3%; Pred. No. 4.1e-49;
Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;
Qy 130 GCGCGCGTGTCTCAAGGACTATGTACACCGTGGGGTTCGCCAGCAAGCCACCATC 189
Db 81 GCTGCGCCCCAAATCAGGAAATGCTGTCCAGTGGGTGTGTACATCACTGTTTCAAGCTT 140
Qy 190 CTTGGGAAGAGCGGTCACTGTCAGCGGCGCCAAACACAGCATCGGGAAGCAGACCGCCTTG 249
Db 141 CTTGGGAAGAGT 200
Qy 250 GAACTGGCCAGAGAGGAGGAGCAACATCATCTGGCTCCGAGACATCAAGAGTGTGAG 309
Db 201 GAGCTGGCTCAGAGAGGAGCTCGAGTATATTAGTCTGCCGGATGTGGAAGAGGGGAA 260
Qy 310 GCGGAGCAAGGAGCATCGCGGGGAGACCTCAATCAACATGTCAACGCCGGGACCTG 369
Db 261 TTGTGGCGCAAGAGATCCAGACACGAGGAAACAGCAGGTGTGGTGGGAAACTG 320
Qy 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTTCAGCAAAAGATCATTAAGAGGAG 429
Db 321 GACCTGTCTGATTAAGTCTATTCGAGCTTTTGTAAAGGGCTTCTTACGTGAGGAAAG 380
Qy 430 CGAGTGGACATTTCTAATCAACAAACGCGGTGTGATCGGTGCGCCCACTGGACCCAG 489
Db 381 CACCTCCACGTTTGTATCAACAAATCAGAGAGTATGTGTCTTCCCTCGCA 440
Qy 490 GAGGGTTTCAGATGAGCTTTGGCGTTAACCACTGGGTGCTTCTTCTGACAACTTG 549
Db 441 GATGGCTTGTGATGACATAGGAGTCAACCACTTGGGTGCTTCTTCTTAAACCATCTG 500
Qy 550 CTGCTGGAACAGCTGAAAGCCTCAGCCCTTCCGCGGATCATCAACCTCTCTGCTTGGCC 609
Db 501 CTGTAGAGAACTAAGGAATCAGCCCATCAAGGATAGTAATGTGTCTTCCCTCGCA 560
Qy 610 CATGTTGCTGGGACATAGACTTTGACGACTTGAACCTGAGCAGCAGGAGTATTAACCC 669
Db 561 CATCACTGGAAGGATCCACTTCCATTAACCTGCGAGGCGCA---GAAATTTACATGCA 617
Qy 670 AAAGCCGCTACTGCGCAGAGCAAGCTCGCATCTCTCTTCCACCAAGAGAGTGGACCGG 729
Db 618 GGCCTGGCTTCTGTCAGAGCAAGCTAGCCAACTCTTTCACCCAGGAACTGGCCCGG 677
Qy 730 CGGCTCAAGGCTCTGGTGTGACTGTCAAGCCCTGCAACCCCGCGTGGCCAGGACAGAG 789
Db 678 AGACTAAAGGCTCTGGCGTTACGAGTATTTCTGTACACCTGGCACAGTCCAACTGAA 737
Qy 790 CTGGGCGACACAGCGGCATCCATGCTCCACTTCTCCAGCACCACTCGGCGCCATC 849
Db 738 CTGGTTCGGCACTCATCTTTATGAGATGATGT-----GGTGGCTT 779
Qy 850 TTCTGGCTGTGTCAGAGCCCGAGCTGGCCCGCCAGCCAGCACATACCTGGCCGTG 909
Db 780 TTCTGCTTTTTCATCAAGACTCTCAGCAGGAGCCAGACAGCCCTGCACTGTGCCTTA 839
Qy 910 GCGAGGAACCTGGCGATGTTTCGGAAGTACTTCGATGACTCAACAGAGAGCCCGG 969
Db 840 ACAGAGGCTTTGAGATTTAAGTGGGAATCATTTAGTACTGTCTATGTGGCATGGGTC 899
Qy 970 GCGCCCGAGGTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTGGCCCGCTG 1029
Db 900 TCTGCCCCAAGCTCGTAATGAGACTATAGCAAGCGGCTGTGGGAGCTCAGTTGTGACCTG 959
Qy 1030 GTGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCCGACATTAACCTCTGAGCAG 1089
Db 960 CTGGGCTTCCCAATAGACTAAAGGAGTGGCCAGTGGACCCAGAGAAAGACTGACGAG 1019
Qy 1090 ATTTGAAAG 1098
Db 1020 ACTACACAG 1028

RESULT 5

US-09-232-149A-332
; Sequence 332, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

; APPLICANT: Xu, Jianshun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; FILE OF INVENTION: CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C6

; CURRENT APPLICATION NUMBER: US/09/232,149A

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 332

; LENGTH: 2507

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-232-149A-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;

Best Local Similarity 55.3%; Pred. No. 4.1e-49;

Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 130 GCGCGCGTGTCTCAAGGACTATGTACCGGTGGGGCTTGGCCCAAGCAAGCCACCATC 189
DB 81 GCTGCGCCCAATCAGGAATGCTGTCAGTGGGTGTGTACATCAACTGTTCAGCTT 140
QY 190 CTTGGGAAGCGGTATCTGTCAGGGGGCCCAACACAGGATCGGGAGCAGACCGCTTG 249
DB 141 CTTGGGAAGTAGTGTGGTCTCAGGAGCTAAACAGGTATCGGGAAGGAGACGCCAA 200
QY 250 GAATGCGCCAGGAGAGGCAACATCATCTGGCTTGGCCGACATGGAGAAGTGTGAG 309
DB 201 GAGCTGTCTAGAGAGCTCGAGTATATTAGCTTGGCGGATGTGGAAAGGGGAA 260
QY 310 GCGCAGCAAGGACATCCCGGGGAGACCTCAATCACATGTCAAGCCCGGACCTG 369
DB 261 TTGTTGGCCAAAGAGATCCAGACCACAGCAAGGAGTGTGGTGGCGAAACTG 320
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGAAAGATCATTTGAAGAGGAG 429
DB 321 GACTGTCTGATAGTCTATTCGAGCTTTGCTAAGGCTTCTAGCTAGGAAAG 380
QY 430 CGAGTGGACATTTCAATCAACACCGGGTGTGATGGGTGGCCCGCTGACGACCGAG 489
DB 381 CACCTCCACGTTTGTGATCAACATGCAAGGATGATGTGTCGTACTCGAAGACGCA 440
QY 490 GACGCTTCGAGATGAGTTTGGGTTAAACACCTGGGTCACTTCTTTGACAAACTTG 549
DB 441 GATGCTTTGATGTCACATAGGAGTCAACACCTGGGTCACTTCTTCTTAACTCTG 500
QY 550 CTGCTGGACAAGCTGAAGCCTCAGCCCTTTCGGGATCATCAACCTCTCTGCTGGCC 609
DB 501 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAATGTGTCTTCTCCGCA 560
QY 610 CATGTTGCTGGCAGATAGCTTTGACACTTGAAGTGGAGAGAGAGTATACAC 669
DB 561 CATACCTGGGAAGGATCCATTTCAATCACTGAGGGCGA---GAATCTACATGCA 617
QY 670 AAAGCGGCTACTGCGCAGACAAGCTCGCCATCGTCTTTCAACAGGAGCTGAGCGG 729
DB 618 GGCCTGGCTACTGTACAGCAAGTAGCCCAACATCCTTTCACCCAGGAATGGCCGG 677
QY 730 CGGTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGACCCCGGCTGGCCAGGACAG 789
DB 678 AGACTAAAGGCTCTGGGCTTACGAGCTATTCTGTACACCTGGCACAGTCCAATCTG 737
QY 790 CTGGGACAGACACCGGGATCCATGGCTCCACTTCTCCAGCACACACTCGGCCCATC 849
DB 738 CTGGTTCGCACTCATCTTTCATGAGTGGATGT-----GGTGGCTT 779

RESULT 6

US-09-636-215-332

; Sequence 332, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jianshun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 332

; LENGTH: 2507

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-636-215-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;

Best Local Similarity 55.3%; Pred. No. 4.1e-49;

Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 130 GCGCGCGTGTCTCAAGGACTATGTACCGGTGGGGCTTGGCCCAAGCAAGCCACCATC 189
DB 81 GCTGCGCCCAATCAGGAATGCTGTCAGTGGGTGTGTACATCAACTGTTCAGCTT 140
QY 190 CTTGGGAAGCGGTATCTGTCAGGGGGCCCAACACAGGATCGGGAGCAGACCGCTTG 249
DB 141 CTTGGGAAGTAGTGTGGTCTCAGGAGCTAATACAGTATCGGGAAGGAGACGCCAA 200
QY 250 GAATGCGCCAGGAGAGGCAACATCATCTGGCTTGGCCGACATGGAGAAGTGTGAG 309
DB 201 GAGCTGGCTCAGAGAGAGCTCGAGTATATTAGCTTCCCGGATGTGGAAAGGGGAA 260
QY 310 GCGCAGCAAGGACATCCCGGGGAGACCTCAATCAATCACTGTCAAGCCCGGACCTG 369

Db 261 TTGGTGGCCAAAGAGATCCAGACCAGCAGGGAACCCAGCAGGTGTGGTGGGAATCTG 320
Qy 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGGCAAAAGATCATTTGAAGAGGAG 429
Db 321 GACCTGTCTGATCTAAGTCTATTCGAGCTTTTGGCTAAGGGCTTCTTAGCTGAGGAAA 380
Qy 430 CGAGTGACATTTCTAATCAACAGCGGGTGTGATCGGTGGCCCGCCACTGGACCCAG 489
Db 381 CACCTCCAGCTTTGATCAACATGAGGAGTGTGATGTGCTGCTGCTGCTGCTGCTGCTG 440
Qy 490 GAGCGTTCAGATGAGTTTGGCTTAACCACTGGGTCACTTTCTTTGACAACTTG 549
Db 441 GATGGCTTTGAGATGCACATAGGATCAACCACTTGGGTCACTTCTGCTGCTGCTGCTG 500
Qy 550 CTGCTGCAAGCTGAAGCTCAGCCCTTCGCGGATCATCACTCTGCTGCTGCTGCTGCTG 509
Db 501 CTGCTGCAAGCTGAAGCTCAGCCCTTCGCGGATCATCACTCTGCTGCTGCTGCTGCTG 560
Qy 610 CATGTTGCTGGCAGATAGCTTTGAGCTTGAACCTGGCAGAGGAGTAAATACACC 669
Db 561 CATCACTGGGAGGATCCATTTCCATACCTGCAGGGCA---GAAATTCATGATGCA 617
Qy 670 AAAGCCGCTTATGCGAGAGAGCTGCGCATGCTCTTTCACCAAGGAGCTGAGCCGG 729
Db 618 GGCTTGGCTTACTGTACAGCAAGCTAGCAACATCTCTTCCACCCAGGAACCTGGCCCG 677
Qy 730 CGGCTGCAAGCTCTGTGTGAGTGTCAACGCGCTGCACCCCGGCTGCAGGACAG 789
Db 678 AGACTAAAGGCTCTGCGGTAGACGTATTTCTGTACACCTGCGACAGTCCATCTGAA 737
Qy 790 CTGGGACAGACACGGGCACTCCATGCTCCACCTTTCCAGCACCACTGCGGCCCATC 849
Db 738 CTGGTTCGGCACTCATCTTTTCATGAGATGATGT-----GGTGGCTT 779
Qy 850 TTCTGGCTGTGATGAGGAGGAGTGGCCGAGGCTTTGGGCTGAAAGTGGCCGCTG 909
Db 780 TTCTCTCTTTTCATCAAGATCTCTCAGCAGGAGCCAGACCACTGCACTGTGCTTAA 839
Qy 910 GCGAGGAACTGGCGGATGTTTCCGGAAGTACTTCGATGAGTCAAAACAGAGGCCCG 969
Db 840 ACAGAGGCTTGAGATTTCAAGTGGGAATCAATTCAGTACTGTGATGGCATGGGTC 899
Qy 970 GCGCCGAGCTGAGGATGAGGAGTGGCCGAGGCTTTGGGCTGAAAGTGGCCGCTG 1029
Db 900 TCTGCGCAAGCTCGTAATGAGCTATAGCAAGGCGGCTGTGGACGCTGAGTGTGACCTG 959
Qy 1030 GTGGCTTAGAGCTCCCTCTGTGAGGAGCAGCCCTCCCGCAGATAACCTCTGAGCAG 1089
Db 960 CTGGGCTCCCAATAGACTAACAGGAGTGCAGTTGGACCCCAAGAGAGACTGCAGCAG 1019
Qy 1090 ATTGAAAG 1098
Db 1020 ACTACACAG 1028

RESULT 7
US-09-685-166A-332
; Sequence 332, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Asrar A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2507
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;
Best Local Similarity 55.3%; Pred. No. 4.1e-49;
Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

Qy 130 GCCCGCTGTGCTCAAGGACTATGTCAACGGTGGGCTTGGCCAGCAAGGCCCATC 189
Db 81 GCTGGCCCCAAATCAGGAAATGCTGTCCAGTGGGTGTATCATCACTGTTCACTT 140
Qy 190 CCTGGGAAGCGTCTATCGTGACGGGCGCAACACAGGATCGGGAAGCAGCCCTTG 249
Db 141 CCTGGGAAGTAGTGTGTGTACAGGAGCTAATACAGGTATCGGGAAGGAGCAGCCAAA 200
Qy 250 GAACTGGCCAGGAGAGGCAACATCATCTCGTCCCTGCGCAGACATCGGGAAGTGTGAG 309
Db 201 GAGCTGGCTCAGAGAGAGCTCGAGTATATTTAGCTTGGCGGATGTGGAAAGGGGAA 260
Qy 310 GCGGAGCAAAAGGACATCCGGGGGAGACCTCAATCACTGTCAAGCCCGGACCTG 369
Db 261 TTGTGGCCAAAGAGATCCAGACCAGCAGGAAACAGCAGGTGTGGTGGCGAAACTG 320
Qy 370 GACTTGGCTTCCCTCAAGTCTATCGGAGTTTCCAGCAAGATCAATGAAGAGAGAG 429
Db 321 GACCTGTCTGATCTAAGTCTATTCGAGCTTTTCTGAGGCTTCTTAGCTGAGGAAAG 380
Qy 430 CGAGTGGACATTTCTAATCAACACCGGGTGTGATGGGTGCGCCCTGACCCAGCAG 489
Db 381 CACCTCCAGCTTTTGTATCAACATGAGGAGTGTGATGTGCTGCTGCTGCTGCTGCTG 440
Qy 490 GAGGCTTCGAGATGAGTGTGGGTTAACACCTGGTCACTTTCTCTTCAAACTTG 549
Db 441 GATGCTTTGAGATGCAATAGGAGTCAACCACTTGGTCACTTCTCTTCAACCCATCTG 500
Qy 550 CTGCTGGCAAGCTGAAAGCCTCAGCCCTTTCGCGGATCATCAACCTCTGCTGCTGCTG 609
Db 501 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAAATGTCTTCTGCTGCA 560
Qy 610 CATGTTGCTGGCAGATAGCTTTGACGACTTGAACCTGGCAGAGGAGGAGTAAACACC 669
Db 561 CATCACTGGGAAGGATCCATTCATTAACCTGCGAGGCGA---GAAATTCATGATGCA 617
Qy 670 AAAGCGCTTACTGCGAGCAAGCTCGCCATCGCTCTTTCACCAAGGAGCTGAGCCGG 729
Db 618 GGCCTGGCTTACTGTGCAAGGAGTACGCAACATCTCTTTCACCCAGGAACCTGGCCCG 677
Qy 730 CGGCTGCAAGCTCTGTGTGAGTGTCAACGCGCTGCAACCCCGGCTGCAGGAGCAG 789
Db 678 AGACTAAAGGCTCTGCGGTACGAGCTATTTCTGTACACCTGCGCAGCTGCAATCTGAA 737
Qy 790 CTGGGACAGACACGGGATCCATGCTCCACCTTCTCCAGCACCACTCGGGGCCCATC 849
Db 738 CTGGTTCGGCACTCATCTTTTCATGAGATGAGTGT-----GGTGGCTT 779
Qy 850 TTCTGGCTGTGATGAGGAGGAGTGGCCGAGGCTTTGGGCTGAAAGTGGCCGCTG 909
Db 780 TTCTCTCTTTTCATCAAGACTCTCAGCAGGAGCCAGACCACTGCACTGTGCTTAA 839

QY 910 GCGAGGAACTGGCGGATGTTTCCGAAAGTACTTCCATGACTCAACAGAGGCCCG 969
 Db 840 ACAGAGGCTCTGAGATCTTAAGTGGATCATTTTCACTGACTGTCTGCGGCTG 899
 QY 970 GCGCCGAGGCTGAGGATGAGGAGTGGCCGAGGCTTTGGGCTGAAAGTCCCGCTG 1029
 Db 900 TCTGCCAAGCTCGTAATGAGACTATAGCAAGGGGCTGTGGGACGTGAGTGTG 959
 QY 1030 GTGGGCTTAGAGGCTCCCTCTGTGAGGAGGAGCGCCCTCCCGAGATACCTCTGAGCAG 1089
 Db 960 CTGGGCCCTCCCAATAGACTAACAGGAGTGGCAGTTGGACCCAGAGAGAGACTGCAGCAG 1019
 QY 1090 ATTGAAAG 1098
 Db 1020 ACTACACAG 1028

RESULT 8
 US-09-688-489-332
 ; Sequence 332, Application US/09688489
 ; Patent No. 6664377
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 ; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.427D2
 ; CURRENT APPLICATION NUMBER: US/09/688,489
 ; CURRENT FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 338
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 332
 ; LENGTH: 2507
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-688-489-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;
 Best Local Similarity 55.3%; Pred. No. 4.1e-49;
 Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 130 GCGCCGCTGCTCAAGGACTATGTCACGGTGGGGCTTGCCTCCAGTGGGGTGTACATCACTTTCAGCTT 140
 Db 81 GCTGCGCCCAATACAGAAATGCTGTCCAGTGGGGTGTACATCACTTTCAGCTT 140
 QY 190 CTTGGGAAGACGCTCATCTGTGACGGCGGCAACACAGGATCGGAAGCAGACCGCTTG 249
 Db 141 CTTGGGAAGTACTTGTGTACAGAGCTATACAGGTATCGGAGGAGACAGCCAAA 200
 QY 250 GAATGCGCAGGAGAGGAGGCAACATCATCTGCGCTGCGGAGACATGGAGAGTGTGAG 309
 Db 201 GAGCTGGCTCAGAGAGGAGCTCAGTATATTTAGCTTGGCGGATGTGAAAAGGGGAA 260
 QY 310 GCGGAGCAAGACATCCGCGGGAGACCTCAATCACATGTCAACCGCGGACCTG 369
 Db 261 TTGGTGCCAAAGATCCAGACACAGAGGACACAGAGGTGTGTGGGAACTG 320
 QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTCCAGCAAGATCATTAAGAGAGGAG 429
 Db 321 GACTGTCTGATATAAGTCTATTCGAGCTTTTGTAAAGGGCTTCTTAGCTGAGGAAAG 380
 QY 430 CGAGTGACATTTCTATCAACACGCGGGTGTGATGGGTGCGCCACCTGGACCCAG 489
 Db 381 CACTCCACCTTTTGAATCAACATGCGAGGATGATGTGCTGCTGAGACAGCA 440
 QY 490 GACGGCTTCGAGATGAGTTTGGGTTTAAACCTGGGTCACTTTCTTTGACAACTTG 549
 Db 441 GATGGCTTTGAGATGACATAGAGTCAACCACTGGGTCACTTTCTCTCAACCCATCTG 500
 QY 550 CTGCTGACAGCTGAAGGCTCAGCCCTTCCGGATCATCAACTCTGCTCCCTGGCC 609

Db 501 CTGTAGAGAACTAAGGATCAGCCCATCAAGGATAGTAATGTGTCTTCCCTCGCA 560
 QY 610 CATGTTGCTGGCACATGACTTTTCAAGCTTTGAACTGGCAGCAGAGGAGTATTAACACC 669
 Db 561 CATCACTGGGAAGGATCCACTTCCATAAAGCTTGCAGGGCGA---GAAATTTCTACAATGCA 617
 QY 670 AAAGCCGCTACTTGCAGAGCAAGCTCGCCATCTCTTCCACCAAGGAGCTGAGCCGG 729
 Db 618 GGCCTGGCTTACTGTTCACAGCAAGTACGCAACATCTTCTTCCAGGAACTGCCCCGG 677
 QY 730 CGGCTCAAGGCTCTGGTGTGACTGTCAAGCCCTGACCCCGGCTGGCCAGGACAGAG 789
 Db 678 AGACTAAAAGGCTCTGGCGTTACGAGCTATTCTGTACACCTTGGCAGCTCCAAATCTGAA 737
 QY 790 CTGGGAGACACAGCGGCTATCCATGCTCCACTTCTCCAGCAGCACACACTCGGGGCCATC 849
 Db 738 CTGGTTCCGCACTCATCTTTTCATGATGATGT-----GGTGGCTT 779
 QY 850 TTCTGGCTGTGCTCAAGAGCCCGAGCTGGCCCGCCAGCCAGCACATACCTTGGCCGTG 909
 Db 780 TTCTCTTTTTCATCAAGACTCTCTCAGCAGGAGCCAGCAGCAGCTGCACTGTGCTTTA 839
 QY 910 GCGGAGAACTGGGATGTTTCCGAAAGTACTTTCGATGGACTCAACAGAGGAGCCCG 969
 Db 840 ACAGAGGCTTGTGAGATTCTAAGTGGGAATCATTTTCACTGACTGTCTGTCATGGGTC 899
 QY 970 GCGCCGAGGCTCAGGATGAGGAGTGGCCCGAGGCTTTGGCTGAAAGTGGCCCTG 1029
 Db 900 TCTGCGCCAAAGCTGTATGAGACTATAGCAAGGCGCTGTGGAGCTGCTGCTGACCTG 959
 QY 1030 GTGGGCTTAGAGCTCCCTCTGTGAGGAGCAGCCCTCCCGAGATAACCTCTGAGGACAG 1089
 Db 960 CTGGGCTCCCAATAGACTAAACAGGAGTGGCCAGTGGACCCCAAGAGAAAGACTGACAGCAG 1019
 QY 1090 ATTGAAAG 1098
 Db 1020 ACTACACAG 1028

RESULT 9
 US-08-464-400-1
 ; Sequence 1, Application US/08464400
 ; Patent No. 5786204
 ; GENERAL INFORMATION:
 ; APPLICANT: HE, ET AL.
 ; TITLE OF INVENTION: Human Prostatic Specific Reductase
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA: US/08/464,400
 ; FILING DATE: Concurrently
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FERRARO, GREGORY D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-228
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-464-400-1

Query Match 12.9%; Score 233.2; DB 1; Length 1086;
Best Local Similarity 55.8%; Pred. No. 8.7e-46;
Matches 498; Conservative 0; Mismatches 373; Indels 21; Gaps 2;
QY 130 GCCCGCGTGTCTCAAGGACTATGTCACCGTGGGGCTTGCACAGCAAGCCACCCTC 189
DB 67 GCTGCGCCCAATCAGAAATGCTCTCAGTGGGGTGTATCATCACTCTTCAGTT 126
QY 190 CTGGGAAGACGGTCTCTGACGGGGCCCAACAGGAGATCGGAGACAGCCGCTTG 249
DB 127 CTGGGAAGTAGTTGTGTGTACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCAAA 186
QY 250 GAATCGCCAGGAGAGGAGCAATCATCTGGCTGCGGAGACATGAGAGAGTGAG 309
DB 187 GAGTGGCTCAGAGAGAGCTCAGTATATTAGCTTGGGGATGTGAAAGGGGAA 246
QY 310 GGGGAGCAATCTAATCAACACGGGGAGACCTCAATCACTGTCAACCCCGGCACTG 369
DB 247 TTGGTGCCAAAGAGATCCAGACCACGAGGAAACGAGTGTGGTGGGAAACTG 306
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTAAGAGGAG 429
DB 307 GACTGTCTGATCTAAGTCTATTTCAGCTTGGCTAAGGGCTTCTTAGCTGAGGAAAG 366
QY 430 CGAGTGGACATTTCTAATCAACACGGGGTGTATCGGTGCCCCACCTGGACCCAG 489
DB 367 CACTCCACGTTTGGATCAACATGACGAGTGTATGTCGCTACTCGAAGACAGCA 426
QY 490 GAGGCTTCGAGATGAGTTGGCTTAACCACTGGTCACTTCTCTTGACAACTG 549
DB 427 GATGGCTTTGAGATGACATAGAGTCAACCACTTGGGTCACTTCTCTTAACCACTG 486
QY 550 CTGCTGGCAAGCTGAAAGCTCAGCCCTTTCGGGATCATCAACCTCTCTGCTGGCC 609
DB 487 CTCTAGAGAACTAAGGAATCAGCCCATCAAGGATAGTAATGTGCTTCCCTCGA 546
QY 610 CATGTTGCTGGCACATAGCTTTGAGACTTGAATCGGAGACGAGGAGTATACCC 669
DB 547 CATCACTGGGAAGGATCCACTTCCATAACCTGCGGGCGA---GAAATTTACATGCA 603
QY 670 AAAGCCGCTTACTGCCAGAGCAAGCTCGCCATGCTCTTCAACCAAGGAGCTGAGCCG 729
DB 504 GGCTGGCTACTGTACAGCAAGCTAGCAACATCTCTTCAACCAAGGAGTGGCCCG 663
QY 730 CGGCTCAAGCTCTGGTGTGATGTCAACGCTTGCACCCCGGTGGCCAGGACAGAG 789
DB 664 AGACTAAAGGCTCTGGCGTTAGCGATTTCTGTACACCTTGGCAAGTCCCAATCTGAA 723
QY 790 CTGGGAGACACACGGGCACTCCATGCTCCACCTTCTCCAGACCACTCGGGCCCATC 849
DB 724 CTGGTTCGGCACTCATCTTTTCATGAGTGA-----TGTTGGGCTT 765
QY 850 TTCTGGTGTGTGTAAGAGCCCGAGCTGGCCGCCAGCCAGCCAGCATACCTTGGCCGTG 909
DB 766 TTCTCTTTTTCATCAAGACTCTCAGCAGGAGCCAGCAGGCTGCACTGTGCTTGA 825
QY 910 GCGGAGAACTGGGGATGTTCCGGGAAGTACTTCGATGGACTCAACAGAGGCCCCG 969
DB 826 ACAGAAGTCTTGAGATTTAATGGGAATCATTTGAGTGACTGTGATGGCATGGGTC 885
QY 970 GCCCCGAGGCTGAGGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTG 1021
DB 886 TCTGCCCAAGCTCGTAAATGAGATATAGCAAGCGGCTGTGGGAGCTCATTTG 937

RESULT 10
US-08-875-273A-1
; Sequence 1, Application US/08875273A
; Patent No. 6106829
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Prostatic Specific Reductase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,273A
; FILING DATE: Concurrently
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-875-273A-1

Query Match 12.9%; Score 233.2; DB 3; Length 1086;
Best Local Similarity 55.8%; Pred. No. 8.7e-46;
Matches 498; Conservative 0; Mismatches 373; Indels 21; Gaps 2;
QY 130 GCCCGCGTGTCTCAAGGACTATGTCACCGTGGGGCTTGCACAGCAAGCCACCCTC 189
DB 67 GCTGCGCCCAATCAGAAATGCTCTCAGTGGGGTGTATCATCACTCTTCAGCTT 126
QY 190 CTGGGAAGACGGTCTCTGACGGGGCCCAACAGGAGATCGGGAAGGAGACAGCCCTTG 249
DB 127 CTGGGAAGTAGTTGTGTGTACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCAAA 186
QY 250 GAATCGCCAGGAGAGGAGCAACATCATCTGGCTTGGCCAGACATGAGAGAGTGAG 309
DB 187 GAGTGGCTCAGAGAGAGCTCAGTATATTAGCTTGGCGGATGTGAAAGGGGAA 246
QY 310 GCGGAGCAAGGAGACATCCGCGGGAGACCCCTCAATCACTGTCAACGCCCGGCACTG 369
DB 247 TTGGTGCCAAAGAGATCCAGACCACGAGGAAACGAGGAGTGTGGTGGGAAACTG 306
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCACCAAGATCATTTAAGAGGAG 429
DB 307 GACTGTCTGATCTAAGTCTATTTCAGCTTGGCTAAGGGCTTCTTAGCTGAGGAAAG 366
QY 430 CGAGTGGACATTTCTAATCAACAGCCGGGTGTGATGCGGTGCCCCACTGCAACCGAG 489
DB 367 CACTCCAGGCTTGGATCAACATGACGAGGATGATGATGTCGCTACTCGAAGACAGCA 426

QY 490 GACGGCTTCGAGATCGAGTTGGCGTTAAACACCTGGGTCACTTCTCTTGACAACTTG 549
Db |||||
QY 427 GATGCTTTGAGATGCGCATAGGAGTCAACCACTTGGTCACTTCTCTTAACCACTTG 486
Db |||||
QY 550 CTGCTGGACAGCTGAAGCCTCAGCCCTTGGCGGATCATCAACCTCTGTCCTGGCC 609
Db |||||
QY 487 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAAATGTCTCTCCCTCGCA 546
QY 610 CATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGAGAGGAAGTATAACAC 669
Db |||||
QY 547 CATCACCTGGGAAGATCCACTTCCATTAACCTGCGAGGCGA---GAAATCTACAATGCA 603
QY 670 AAAGCCGCTACTGCGCAGAGAGCTCCGCATCGCTCTCTTCAACAAGGAGCTAGCCGG 729
Db |||||
QY 604 GGCCTGGCTTACTGTCACAGCAAGCTAGCCCAACATCTCTTCAACCAGGAATGCCCCGG 663
QY 730 CGGCTGCAAGGCTCTGGGTGACTGTCAACGCCCTGACCCCGCGTGGCCAGGACAGAG 789
Db |||||
QY 664 AGACTAAAGGCTCTGGCGTTACGAGTATTTCTGTACACCTGGCAGTCAATCTGAA 723
QY 790 CTGGCAGACACACGGGATCCATGCTCCACCTTCTCCAGCACACACTCGGSCCCATC 849
Db |||||
QY 724 CTGGTTCGCACTCATCTTTTATGAGATGGA---TGTTGGCTT 765
QY 850 TTCTGGCTGCTGCTCAAGAGCCCGAGCTGCGCGCCAGCCAGCACATACCTGGCCGTG 909
Db |||||
QY 766 TTCTCTTTTCAACAGACTCTCAGCAGGAGCCAGACAGGCTGCACTGTGCTTA 825
QY 910 GCGGAGGAACTGGCGGATGTTTCCGAAAGTACTTCGATGAGCTCAACAGAGGCCCG 969
Db |||||
QY 826 ACAGAGGCTCTTGAATCTTAAGTGGGAATCATTTCACTGACTGTGATGGCATGGTCT 885
QY 970 GCGCCCGAGGCTGAGGATGAGGAGTGGCCCGGAGCTTTGGCTGAAAGTG 1021
Db |||||
QY 886 TCTGCCCAAGCTCTGAATGAGACTATAGCAAGGCGGCTGTGGAGCTCATTTG 937

RESULT 11

US-09-123-386-1

; Sequence 1, Application US/09123386

; Patent No. 6344198

; GENERAL INFORMATION:

; APPLICANT: HE, ET AL.

; TITLE OF INVENTION: Human Prostatic Specific Reductase

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSES: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVE

; CITY: ROCKVILLE

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/123,386

; FILING DATE: JUL-27-1998

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/464,400

; FILING DATE: JUN-05-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Jonathan L. Klein

; REGISTRATION NUMBER: 41,119

; REFERENCE/DOCKET NUMBER: PF150D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1086 BASE PAIRS

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: cDNA

US-09-123-386-1

Query Match

Best Local Similarity 12.9%; Score 233.2; DB 4; Length 1086;

Matches 498; Conservative 0; Mismatches 373; Indels 21; Gaps 2;

QY 130 GCGCGCTGCTCTCAAGACTATGTCAACCGTGGGCTTCCCGCAGCAAGCCCACTC 189
Db 67 GCTGCGCCCAAAATCAGGAAATGCTGTCACTGGGTTGTACATCACTTTCAGCTT 126
QY 190 CTTGGGAAGACGGTTCATCGTACGGCGCCCAACACAGGATCGGGAAGCAGCCCTTG 249
Db 127 CTTGGGAAGTAGTTGTGTGTACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCA 186
QY 250 GAATGCGCAGGAGGAGGCAACATCATCTGCGCTGCCGAGCATGGGAAGTGTGAG 309
Db 187 GAGCTGGCTCAGAGAGGAGCTCGAGTATATTTAGCTTGGCGGATGTGAAAGGGGAA 246
QY 310 GCGGAGCAAAAGGACATCCGCGGGGAGACCTCAATCAACCATGTCAACGCCCGGACCTG 369
Db 247 TTGTTGCGCCAAAGAGATCCAGACCCAGCAGGGAACAGCAGGTGTGTGTCGGAACCTG 306
QY 370 GACTGGCTTCCCTCAAGTCTATCGGAGATTGCGAGCAAAAGATCATTTGAAGAGGAG 429
Db 307 GACTGCTGTGATACTAAGTCTATTGAGCTTGGGCTTAAGGGCTTCTTAGCTGAGGAAAG 366
QY 430 CGAGTGGACATTTAATCAACCAACGCGGTGTGATGCGGTGCCCGACCTGGACCCAGG 489
Db 367 CACTTCCAGTTTGGATCAACATGAGGAGTATGATGTGCTGCTGCTGAGGAGCAGCA 426
QY 490 GAGCGTTCCGATGAGTTTGGCGTTAACCACTGGGTCACTTCTCTTGAACAACCTTG 549
Db 427 GATGGCTTTGAGATGCACATAGGAGTCAACCACTTGGGTCACTTCTCTTAACCCATCTG 486
QY 550 CTGCTGGACAAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCTGCTCTGGCC 609
Db 487 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAAATGTGTCTTCCCTCGCA 546
QY 610 CATGTTGCTGGGCACATAGACTTTGAGACTTTGAGACTGGCAGCAGGAGGAGTATACACC 669
Db 547 CATCACTGGGAAGGATCCACTTCCATAACCTGCGAGGCGA---GAAATTTACAAATGCA 603
QY 670 AAAGCGCCTACTGCGCAGAGCAAGCTCGGCATCGTCTCTTCAACCAAGGAGCTGAGCCGG 729
Db 604 GGCCTGGCTACTGTTCACAGCAAGCTAGCCCAATCTCTTCAACCAGGAATGCGCCCG 663
QY 730 CGGCTGCAAGGCTCTGGTGTGACTGTCAAGCGCCTGCAACCGCGGTGGCCAGGAGCAGAG 789
Db 664 AGACTAAAGGCTCTGGCGTTACGAGTATTTCTGTACACCTGGCAGTCAATCTGAA 723
QY 790 CTGGGCGACATCATCTTTTCATGAGTGA---TGTTGGCTT 765
Db 850 TTCTGGCTGCTGCTCAAGAGCCCGGAGCTGGCGCCAGCCAGCAGCATACCTTGGCCGTG 909
Db 766 TTCTCTTTTCAACAGACTCTCAGCAGGAGCCAGACAGGCTGCACTGTGCTTA 825
QY 910 GCGGAGGAACTGGCGGATGTTTCCGAAAGTACTTCGATGAGCTCAACAGAGGCCCG 969
Db 826 ACAGAGGCTCTTGAATCTTAAGTGGGAATCATTTCACTGACTGTGATGGCATGGTCT 885
QY 970 GCGCCCGAGGCTGAGGATGAGGAGTGGCCCGGAGCTTTGGCTGAAAGTG 1021
Db 886 TCTGCCCAAGCTCTGAATGAGACTATAGCAAGGCGGCTGTGGAGCTCATTTG 937

RESULT 12

PCT-US95-01827A-1
; Sequence 1, Application PC/TUS9501827A
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Prostatic Specific Reductase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01827A
; FILING DATE: Concurrently
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-01827A-1

Query Match 12.9%; Score 233.2; DB 5; Length 1086;
Best Local Similarity 55.8%; Pred. No. 8.7e-46;
Matches 498; Conservative 0; Mismatches 373; Indels 21; Gaps 2;
QY 130 GCGCGCGTCTGCTCAAGGACTATGTCCCGTGGGGTTCGCCAGCAAGGCCACCATC 189
DB 67 GCTGCGCCCAATCAGGAATGCTGTCAGTGGGTGTGTACATCAACTGTTTCAGCTT 126
QY 190 CTTGGGAGACGGTATGTCGGGGCGGCAACAGGATCGGGAGCAGACCGCCTTG 249
DB 127 CTTGGGAAAGTAGTTGTGGTCAAGAGGCTAATACAGGTATCGGGAAGAGACGCCAAA 186
QY 250 GAACTGGCGAGGAGGAGGCAACATCATCTCGGCTCGCGAGATCGGAGAGTGTGAG 309
DB 187 GAGCTGGCTCAGAGGAGCTCGAGTATATTAGTTTCCCGGATGTGGAAGGGGAA 246
QY 310 GCGGAGCAAAAGGACATCGCGGGGAGACCTTCATACCATGTCAACCGCCGACCTG 369
DB 247 TTGGTGGCCAAAGAGATCCAGACCACGAGGGAACCCAGCAGGTGTTGGTGGGAAACTG 306
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGAGCAAAAGATCATTTGAAGAGGAG 429
DB 307 GACCTGTCTGATCTAAGTCTATTTCAGCTTGGGCTAAGGGTCTTTAGCTGAGGAAG 366
QY 430 CGAGTGGACATTCTAATCAACACCGGGTGTGATCGGTTGCCCTCCACTGGACCAACCGAG 489
DB 367 CACCTCCAGTTTGGATCAACAATCAGGAGTGTGTCGCTACTCGAAGACAGCA 426
QY 490 GACGCTTCGATGCTAGTTTGGCGTTTACCACTGGGTCACTTCTTTCACAACTTG 549

DB 427 GATGGCTTTGAGATGCACATAGGAGTCAACCACTTGGGTCACTTCTCTCTAACCCTG 486
QY 550 CTGCTGGAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCTGCTCCCTGGCC 609
DB 487 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAATGTGTCTTCCCTCGCA 546
QY 610 CATGTTGCTGGGCACATACACTTTGAGGACTTGAAGTGGCAGCAGGAAAGTATACACC 669
DB 547 CATCACTGGGAAGGATCCACTTCCATACTTGCAGGGCGA---GAAATTTACATGCA 603
QY 670 AAAGCCGCTACTGCGCAGAGCAAGTTCGCATTCCTCTTCCACCAAGAGTGTGAGCCGG 729
DB 604 GGCCTGGCCTACTGTACAGCAAGCTAGCCAAACATCTCTTACCCAGGAATCGGCCCG 663
QY 730 CGGCTGCAAGGCTCTGGTGTGACTGTCAAGCCCTGCACCCGGGTGSCCAGGACAGAG 789
DB 664 AGACTAAAGGCTCTGGCGTTAGAGGATTTCTGTACACCTGGCACAGTCCAACTGAA 723
QY 790 CTGGGACAGACACACGGGCAATCCATGGCTCCACTTTCACGACCACACTCGGGGCCATC 849
DB 724 CTGGTTGGCACTCATCTTTTCATGATGGA-----TGTGTGGCTT 765
QY 850 TTCTGGCTGCTGGTCAAGAGCCCGAGCTGGCGGCCAGCCAGCACATACCTGGCCGTG 909
DB 766 TTCTCTCTTTTCATCAAGACTCTCTCAGCAGGAGGCCACAGCAGCTGCACGTGCTTA 825
QY 910 GCGGAGGAACTGGCGGATGTTTCCGGAAGTAGTTTCGATGAGTACTCAAAACAGAGGCCCG 969
DB 826 ACAGAGGCTTTGAGATTTCTAAGTGGGAATCATTTTCAGTACTGTCTGTCATGGCATGGTC 885
QY 970 GCGCCGAGGCTGAGGATGAGAGGTTGGCCCGGAGGCTTTGGCTGGAAGTG 1021
DB 886 TCTGCCAAAGCTCGTAATGAGACTATAGCAAGCGGCTGTGGACGTCAATTG 937

RESULT 13

US-09-833-381-933
; Sequence 933, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 933
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-933

Query Match 12.1%; Score 219.6; DB 4; Length 234;
Best Local Similarity 96.2%; Pred. No. 8.7e-43;
Matches 225; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1184 GCGGCGCCATGCCCCGAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGCGCTG 1243
DB 1 GCGGCGCCATGCCCCGAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGCGCTG 60
QY 1244 CAGGTGAGCACTGCCCGGGCTCTGGCTGTTCCGTTCTCTCTGTGCCAGCAGGGGAGA 1303
DB 61 CAGGTGAGCACTGCCCTCGGGCTCTGGCTGTTCCGTTCTCTGTCTGCTGCCATCAAGGAGA 120
QY 1304 GGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGAGGGCT 1363
DB 121 GGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGGCT 180
QY 1364 CTGTGCACTTGCAGGCGCAGTCAAGGAGCCAGCGGTGCTGTCTCGGGGAGGGTT 1417

Db 181 CCGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTTCGGGAGGGTT 234

RESULT 14

US-09-103-840A-2

; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 9.3%; Score 168.2; DB 3; Length 4403765;
Best Local Similarity 54.7%; Pred. No. 2.2e-29;
Matches 357; Conservative 0; Mismatches 293; Indels 3; Gaps 1;
Qy 155 TCACCGGTGGGGCTTGCCCAAGAGCCACATCCCTGGGAAGACGGTCAATCGTGACGG 214
Db 75279 TGACCAATGACTGCCCGACATTCCTGACAGACCGCGCGGACGCTCATCAGG 75338
Qy 215 GCGCCACACAGGATCGGGAAGCAGACCGCTTGGAACTGGCCAGAGAGGAGGCAACA 274
Db 75339 GGGCCAAACCGGACTTGGATTCGAGACCGCGCGAGCTTGCAGCCATCGGTGCACAG 75398
Qy 275 TCATCTGGCTCGCGAGACATGGAGAAGTGTGAGGGCGGAGCAAGACATCCGCGGG 334
Db 75399 TGGTGTGGCTGTGGCAACCTCGACAGGCAAGCGGCGGACGATCACCAGG 75458
Qy 335 AGACCTCAATCACCATGTCAACCGCGGACCTGGACTTGGCTTCCCTCAAGTCTATCC 394
Db 75459 CCACCCCGCGCGGAGTAGAGCTTCAGGAGCTTGACCTGACCTCGCTGGCGTGC 75518
Qy 395 GAGAGTTTGCAGCAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTTAATCAACAACG 454
Db 75519 GCGCGCGCGGACAGCTGAAGTCTGACCAAGCGATCGACCTGATCAACAACG 75578
Qy 455 CGGTTGATCGGGTGGCCCACTGGACCAAGCGAGAGGGTTCGAGATCGAGTTGGCG 514
Db 75579 CCGGGGTGATATATACACCCCGGACAGACCAAGAGAGCGGCTTCGAGATCGATTCGGCA 75638
Qy 515 TTAACCACTGGGTCACTTTCTCTTGACAAACTTGTCTGGACAAAGCTGAAGCTCAG 574
Db 75639 CCAACCACTTGGGCAATTCGGTTGACCGGCTTGTGATGATCGACTGCTCCCGTCG 75698
Qy 575 CCCCTTCGGGATCATCAACCTCTCGTCCCTGGGCCATGTTGTGGGCAATAGACTTG 634
Db 75699 CCGGTTACGAGTGTACCAATCAGACGCTCGGCCATCGCATCCGTCGCGCATCCATT 75758
Qy 635 ACGACTTGAATGGCAGAGGAGTATAACACCAAGCGCCCTACTGCCAGAGCAAGC 694
Db 75759 TCGACGACCTCAGTGGGAACCGCGGTACAGCGGGTGCAGCGCTACGGCAAGCCAGC 75818
Qy 695 TCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTG 754
Db 75819 TCGCCAACTGCTGTTCATTTATGAATTCAGCTCGGTGTAGCACCGGGGGAACCA 75878

Qy 755 TC---AAGCCCTGCACCCCGCGCTGGCCAGGACAGAGCTGGGCGAGACACACG 804
Db 75879 TCGCGTCCGCTGCGCAGCCCGGAGTGTCCAAACACCGAACTGGTCCGCAACATG 75931

RESULT 15

US-09-103-840A-1

; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 9.2%; Score 166.6; DB 3; Length 4411529;
Best Local Similarity 54.5%; Pred. No. 5.4e-29;
Matches 356; Conservative 0; Mismatches 294; Indels 3; Gaps 1;
Qy 155 TCACCGGTGGGGCTTGCCCAAGAGCCACATCCCTGGGAAGACGGTCAATCGTGACGG 214
Db 75300 TGACCAATGACTGCCCGACATTCCTGACAGACCGCGGACGCTCATCAGG 75359
Qy 215 GCGCCACACAGGATCGGGAAGCAGACCGCTTGGAACTGGCCAGAGAGGAGGCAACA 274
Db 75360 GGGCCAAACCGGACTTGGATTCGAGACCGCGGAGCTTGCAGCCATCGTGACACG 75419
Qy 275 TCATCTGGCTCGCGAGACATGGAGAAGTGTGAGGGCGGAGCAAGACATCCGCGGG 334
Db 75420 TGGTGTGGCTGTGGCAACCTCGACAGGCAAGCGGCGGACGATCACCAGG 75479
Qy 335 AGACCTCAATCACCATGTCAACCGCGGACCTGGACTTGGCTTCCCTCAAGTCTATCC 394
Db 75480 CCACCCCGCGGCGGAGTAGAGCTTCAGGAGCTTGACCTGACCTCGCTGGCGTGC 75539
Qy 395 GAGAGTTTGCAGCAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTTAATCAACAACG 454
Db 75540 GCGCGCGCGGACAGCTGAAGTCTGACCAAGCGATCGACCTGATCAACAACG 75599
Qy 455 CGGTTGATCGGGTGGCCCACTGGACCAAGCGAGAGGGTTCGAGATCGAGTTGGCG 514
Db 75600 CCGGGGTGATGATACACCCCGGACAGACCAAGAGAGCGGCTTCGAGATCGAGTTCCGCA 75659
Qy 515 TTAACCACTGGGTCACTTTCTCTTGACAAACTTGTCTGGACAAAGCTGAAGCTCAG 574
Db 75660 CCAACCACTTGGGCAATTCGGTTGACCGGCTTGTGATGATCGACTGCTGCCGTCG 75719
Qy 575 CCCCTTCGGGATCATCAACCTCTCGTCCCTGGGCCATGTTGTGGGCAATAGACTTG 634
Db 75720 CCGGTTACGAGTGTGTCACCATCAGACGCTCGGCCATCGCATCCGTCGCGCAATCCATT 75779
Qy 635 ACGACTTGAATGGCAGAGGAGTATAACACCAAGCGCCCTACTGCCAGAGCAAGC 694
Db 75780 TCGACGACCTCAGTGGGAACCGCGGTACAGCGGGTGCAGCGCTACGGCAAGCCAGC 75839
Qy 695 TCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTG 754
Db 75840 TCGCCAACTGCTGTTCATTTATGAATTCAGCTCGGTGTAGCACCGGGGGAACCA 75899
Qy 755 TC---AAGCCCTGCACCCCGCGCTGGCCAGGACAGAGCTGGGCGAGACACACG 804

Db 75900 TCGGTCGCGTCGCCACCCGGGAGTGTCCACACCCGAGTGTCCGCAACATG 75952

Search completed: June 23, 2004, 14:47:06
Job time : 160 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: June 23, 2004, 11:04:49 ; Search time 21 Seconds
(without alignments)
1516.162 Million cell updates/sec

Title: US-10-015-393a-116
Perfect score: 1695
Sequence: 1 MSRYLLPLSALGTVAGAAVL.....ESARLVGLEAPSVREQLPLR 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	33.4	303	2 E70848	probable oxidoredu
2	534	31.5	311	2 H70829	hypothetical prote
3	531.5	31.4	304	2 T44727	probable oxidoredu
4	515	30.4	320	2 S42651	hypothetical prote
5	513.5	30.3	336	2 H75255	oxidoreductase, sh
6	497	29.3	321	2 T02520	probable oxidoredu
7	487.5	28.8	350	2 T48275	hypothetical prote
8	485.5	28.6	311	2 A20221	hypothetical prote
9	485	28.6	323	2 E87298	hypothetical prote
10	475.5	28.1	317	2 C70863	hypothetical prote
11	457.5	27.0	316	2 D84206	probable oxidoredu
12	456	26.9	317	2 T10561	hypothetical prote
13	451	26.6	309	2 C83017	probable short cha
14	447.5	26.4	332	2 T13447	hypothetical prote
15	438.5	25.9	301	2 AE3195	dehydrogenase Adu
16	437	25.8	333	2 T19314	hypothetical prote
17	428	25.3	339	2 T41570	hypothetical prote
18	414	24.4	311	2 T37155	probable oxidoredu
19	402	23.7	312	2 T37150	probable oxidoredu
20	390.5	23.0	294	2 T05381	hypothetical prote
21	382.5	22.6	204	2 T46363	hypothetical prote
22	381	22.5	400	2 C75365	daunorubicin C-13
23	364	21.5	329	2 A12023	proteobacteri
24	362.5	21.4	312	2 D83689	hypothetical prote
25	357	21.1	297	2 S19842	probable oxidoredu
26	356	21.0	397	2 S71468	proteobacteri
27	353.5	20.9	298	2 A47089	probable oxidoredu
28	349.5	20.6	291	2 G97327	short-chain alcoho
29	345.5	20.4	400	2 S20941	proteobacteri

30	345	20.4	339	2 B86906	oxidoreductase yxd
31	342	20.2	388	2 S04783	proteobacteri
32	342	20.2	398	2 T33973	hypothetical prote
33	341.5	20.1	296	2 D82515	ketoreductase Xp27
34	339	20.0	388	2 S39394	proteobacteri
35	338.5	20.0	401	2 T08936	proteobacteri
36	338	19.9	398	2 JC4146	proteobacteri
37	336	19.8	322	2 T43931	proteobacteri
38	336	19.8	329	2 T15910	hypothetical prote
39	331	19.5	313	2 S08406	proteobacteri
40	329	19.4	401	2 T00897	proteobacteri
41	328.5	19.4	400	2 S30167	proteobacteri
42	326.5	19.3	395	2 S52285	NADPH2 dehydrogena
43	325	19.2	322	2 S76636	hypothetical prote
44	317.5	18.7	322	2 T04022	hypothetical prote
45	312	18.4	302	2 H70523	hypothetical prote

ALIGNMENTS

RESULT 1
E70848
probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: E70848
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70848
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-303 <COL>
A:Cross-references: GB:AL021428; GB:AL123456; NID:93261514; PIDN:CAA16249.1; PID:92808
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0068
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:15-208/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match	33.4%	Score 566;	DB 2;	Length 303;
Best Local Similarity	43.9%;	Pred. No. 1.3e-37;		
Matches 133;	Conservative 47;	Mismatches 101;	Indels 22;	Gaps 8;
QY	34	ATIP-----GKTIVITGANTGIGKQTAL	ELARRGNNIILACRMEKCEAAAKD	IRGETLNHH 90
Db	7	ADIPDQGTAVITGANTGLGFTAAALAA	GAHVVLAVRNLDKQKAAARITEATFGAE	66
QY	91	VNARHLDLASLSIRFEAAKIIEEERVDIL	NNAGVRCPHWTTEDEGFEMQFGVNHLGH	150
Db	67	VELQELDLTSLASVRAAAQLKSDHORIDL	LLNNAGVWYTPQTADGFMQFGTNHLGH	126
QY	151	FLTLNLLDKLKASAPSRINLSSLAH-VAG	HDIDFDLNNWQTRKYNKTAAYCOSKLAIVL	209
Db	127	FALTGLLIDRLLPVAGSRVVTSSVGHRI	RAALHFDDDLQWE-RRYRVAAYGQAKLANLL	185
QY	210	FTYKELRRRGGGVWVN-ALHPGVARTEL	GRHTGTHGHSFTSTTLGPIFWLLVKSPELAA	268
Db	186	FTYELQRLAPGGTTTAVASHFGVSNTEV	-----VRNMPRLVAVAAIILAPLMQDAELGA	240
QY	269	QPSTYLAVARELADVSGKYF--DGL-----	KOKAPAPEAEDEEVARLWAEARLVGL	319
Db	241	LPT--LRAATDPAVRGGQYFGPDGFGFGE	IRGYPKVAVASSAQSHDEQLQRLWAVSEELTGV	298
QY	320	EAP	322	
Db	299	VIP	301	

RESULT 2

H70829
Hypothetical protein Rv0439c - Mycobacterium tuberculosis (strain H37Rv)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C/Accession: H70829
R/Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: H70829
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-311 <COL>
A/Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PID:CAAL17396.1; PID:g290951
A/Experimental source: strain H37Rv
C/Genetics:
A/Gene: Rv0439c
C/Suprafamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
P;22-216/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 31.5%; Score 534; DB 2; Length 311;
Best Local Similarity 43.3%; Pred. No. 4.9e-35;
Matches 132; Conservative 42; Mismatches 105; Indels 26; Gaps 10;

QY 32 SKATIP--GKTIVTGANTGIGKQTALRLARRGNIILACRDMKECEAAKDIRGETLN 88
DB 12 SAADVPQSGRVVVTGANTGIGVHTAAVADRGAHVVLAVRLNLEKGNARARIMARPG 71
QY 89 HHVNAHLDLASLKSIREFAAKIIEBERVDILINNAGVMRCPTHWTEDGFEMQFQVNH 148
DB 72 AHVTLLQDLCLSDVRAADALRTAYPRIDVLINNAGVMWTPKQVTKDGFELQFGTNHL 131
QY 149 GHFTLLNLLDKLASAPSRINLSLAH-VAGHIDFDDLNQTRKYNKTAAYCQSKLAI 207
DB 132 GHFALTGLVDHMLPVGSGRVVTVSSQCHRIHAHIEDDLQWE-RRYRNVAAVQAKLAN 190
QY 208 VLFTKELSRRL--QGSGVTVNALHPGVARTELGRHTG--IHGSTFSSFTTLGPFWLLVKS 263
DB 191 LLFTVELQRLGEAGKSTIAVAHPGSGNTLRLNLPRLRP--VATVLGP--LLFQS 244
QY 264 PELAAQSTYLAVAEELADVSGKYF--DGLKQKAPAP-----EAEDEVARLLWAESA 314
DB 245 PEMGALPT--LRAATDPTTGGQYYPGDPGFGEORGEKPKVQSSAQSHDKQLQRLWTVE 302
QY 315 RLVLG 319
DB 303 ELTGV 307

RESULT 3

T44727
Probable oxidoreductase [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
C/Accession: T44727
R/James, K.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
A/Reference number: 222831
A/Accession: T44727
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-304 <JAM>
A/Cross-references: EMBL:AL035159; PIDN:CAA22691.1
A/Experimental source: cosmid B1450
C/Genetics:
A/Note: MLCB1450.07
C/Suprafamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 31.4%; Score 531.5; DB 2; Length 304;
Best Local Similarity 43.0%; Pred. No. 7.5e-35;
Matches 132; Conservative 45; Mismatches 101; Indels 29; Gaps 10;

QY 34 ATIP--GKTIVTGANTGIGKQTALRLARRGNIILACRDMKECEAAKDIRGETLN 90
DB 7 ADIPDQTRGVAITGANTGLGYTALALAEHGAHVLAVRNLDRKGDAAARITATSQNN 66
QY 91 VNARHLDLASLKSIREFAAKIIEBERVDILINNAGVMRCPTHWTEDGFEMQFQVNH 150
DB 67 VALQELDLASLESVRAAAKQLRSYDHIDLLINNAGVMWTPKSTTKDGFELQFGTNHL 126
QY 151 FLLTNLLDKLASAPSRINLSLAH-VAGHIDFDDLNQTRKYNKTAAYCQSKLAI 209
DB 127 FAFTGLLDRLLPVIGSRVITVSSLSHRLFAHIDHFNLOWEC-NYNRVAAYGQSKLAN 185
QY 210 FTKELSRRLQSGVTVN-ALHPGVARTELGRHTGHTGFTSFTTLGPFI--WLLVKSP 264
DB 186 FTYELQRLATPQTTIAVAHPGSGRTELRTL-----PALIAIFSVAEELFLTQDA 237
QY 265 ELAAQSTYLAVAEELADVSGKYF--DGLKQ-----KAPAEAEDEVAR--RLWASSAR 315
DB 238 ATGALPT--LRAATDAAVLGGYYPGDPGFABIRGHPKVASNGKSHDVRQLRLWAVSEE 295
QY 316 LVGLEAP 322
DB 296 LTGVVYP 302

RESULT 4

S42651
Hypothetical protein - rape
C/Species: Brassica napus (rape)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C/Accession: S42651
R/Coupe, S.A.; Taylor, J.E.; Isaac, P.G.; Roberts, J.A.
Plant Mol. Biol. 24, 223-227, 1994
A/Title: Characterization of a mRNA that accumulates during development of oilseed rape
A/Reference number: S42651; MUID:94154236; PMID:8111020
A/Accession: S42651
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-320 <COU>
A/Cross-references: EMBL:X74225; NID:g456719; PIDN:CAB58175.1; PID:g6065752
C/Suprafamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
P;34-235/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 30.4%; Score 515; DB 2; Length 320;
Best Local Similarity 42.8%; Pred. No. 1.7e-33;
Matches 125; Conservative 50; Mismatches 93; Indels 24; Gaps 8;

QY 40 TVIVTGANTGIGKQTALRLARRGNIILACRDMKECEAAKDIRGETLNHHVNAR--- 95
DB 35 TAITTGTSGIGLEAARVLCGRGAHVIIASRNTK---AANDSKEMILQMPNARIDCLQ 90
QY 96 LDLASLKSIREFAAKIIEBERVDILINNAGVMRCPTHWTEDGFEMQFQVNHGFLTN 155
DB 91 LDLSSIKSVSRPIHQFALNVPNLINNAGVMFCFQLSEDGIESQFATNHHGFLTN 150
QY 156 LLLDLKLKSA-----PSRLINLSLAHVAGH---IDFDDLNQTRKYNKTAAYCOSKLAI 207
DB 151 LLLDKKMSARSGEGRIIVNLSIAHYTYTTEGIMFYIN-DPRYSEKAYGOSKLAN 209
QY 208 VLFTKELSRRLQSGV--TVNALHPGVARTELGRHTGHTGFTSFTTLGPFWLLVKSP 265
DB 210 LLHSNALSRKLQEGVNITINSVHPGLITTLFRHSGGLGMAVLKAMS----PFLWKNIPQ 265
QY 266 LAAQSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEVARLLWAESARLV 317
DB 266 GAA-TTCYVALHFDLKDVTGKYFADCNVTPPSNFATDTTLADKLWDFSIKV 316

RESULT 5

H75255
 oxidoreductase, short-chain dehydrogenase/reductase family - Deinococcus radiodurans (sb
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: H75255
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036996; PMID:10567266
 A:Accession: H75255
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-336 <WHI>
 A:Cross-references: GB:AE000513; GB:AE0002089; PIDN:AAE12130.1; PID:g646041
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2595
 A:Map position: 1
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 30.3%; Score 513.5; DB 2; Length 336;
 Best Local Similarity 37.9%; Pred. No. 2.3e-33;
 Matches 135; Conservative 41; Mismatches 121; Indels 59; Gaps 7;
 QY 1 MSRYLLP-----LSALGTGAGAAVLLKDYVTGGACPSKATIPGKTVITG 45
 DB 1 MARRELPSMTHGSSQSDPRISFLAPRAAAEVVRG-----VDLKGKTAVTG 50
 QY 46 ANTGGKQTALRLARGGNIIACRDMEKCEAAKDIRGETLNHHVNAHLDLASLSIR 105
 DB 51 GASGIGTETARALLAGAVILPVRDRAGKRVAAELRQST--GGTVELVDLDGLASVR 109
 QY 106 EPAAKIIEEERVDILINNAGVRCPHWTTEDGFEMQFGVNHGFLHFLTLNLLDKLAKSA 165
 DB 110 RGAERQLAPRIHILINNAGVWATPQSTVDGFTQGTNHLGHFLTLRELLPALMAA 169
 QY 166 PSRIINLSLAHVAGHIDPDDLWQTKRYNTKAAVCOQSLAIVLFTKELSRLOGSGVT 225
 DB 170 PARVVALTSSGHRSDIYWDLLNFERPYPDWDAYGQSKTANALPAVLGTORYADQGLTA 229
 QY 226 NALHPGVARTLGRHTGI-----HGTFSTSTLGPFLWLLVKSPELLAQPSTYL 274
 DB 230 NAVHGGWITGLQKVFVLDQRMGWQDEHG-----TLNPFV-----KTPAEGASTSWA 279
 QY 275 AVAELADVSGKYFDGLKQKAP-----APEAEDEEVARRLWAESARLVG 318
 DB 280 ATSPQLYGVGGLFLEDLQSTPLDESAPNPLFGYKPYALDHESARRLWALSEALVG 335

RESULT 6
 T02520
 probable oxidoreductase [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein F13M22.4
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001
 C:Accession: T02520; A84794
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, June 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
 A:Reference number: Z14677
 A:Accession: T02520
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-321 <ROU>
 A:Cross-references: EMBL:AC004694; NID:g3236234; PID:g3236237
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84794
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-321 <STO>
 A:Cross-references: GB:AE002093; NID:g3236237; PIDN:AAE12130.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g37540; F13M22.4
 A:Map position: 2
 A:Introns: 40/1; 117/2; 144/1; 195/2; 221/3; 250/1; 265/3
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 29.3%; Score 497; DB 2; Length 321;
 Best Local Similarity 40.8%; Pred. No. 4.6e-32;
 Matches 119; Conservative 52; Mismatches 97; Indels 24; Gaps 8;
 QY 40 TVIVTGANTGIGKQTALRLARGGNIIACRDMEKCEAAKDIRGETLNHHVNAH 95
 DB 35 TAITGTGTGIGLEAAARVLAMGAHVIIAARPK-----AANESKEMILQMNPNARVDYLQ 90
 QY 96 LDLASLSIREFAAKIIEEERVDILINNAGVRCPHWTTEDGFEMQFGVNHGFLHFLTN 155
 DB 91 IDVSSIKSVRSFVDQFLALNVLNINLNNAGVWFCFFKLTEDGIESQFATNHHGFLTN 150
 QY 156 LLDLKLKASA-----PSRIINLSLAHVAGH-----IDFDLWQTKRYNTKAAVCOQSLAI 207
 DB 151 LLDLKKMSTARESGVQGRIVNLSIAHTYTYSEGKIFQGIN-DPAGYSERRAYGQSKLN 209
 QY 208 VLFTEKLSRLQSGV--TVNALHPGVARTLGRHTGIHGTFSTSTLGPFLWLLVKSPE 265
 DB 210 LLSNALSRRLQEBGVNIIINSVHFGVLTNLFVSGFSKMYFRATPF--LFW--KNIP 264
 QY 266 LAQPTTYAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLWAESARLV 317
 DB 265 QGAATTCYVALHPDLRGVTKYFGDCNIVAPSKFATNNSLADKLMDPSVFLI 316

RESULT 7
 T48275
 hypothetical protein T22P11.130 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
 C:Accession: T48275
 R:Bayan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z44490
 A:Accession: T48275
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <BEV>
 A:Cross-references: EMBL:AL162971
 A:Experimental source: cultivar Columbia; BAC clone T22P11
 C:Genetics:
 A:Map position: 5
 A:Introns: 40/1; 136/2; 163/1; 214/2; 240/3; 269/1; 284/3
 A:Note: T22P11.130
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.8%; Score 487.5; DB 2; Length 350;
 Best Local Similarity 38.2%; Pred. No. 2.9e-31;
 Matches 118; Conservative 54; Mismatches 98; Indels 39; Gaps 8;
 QY 40 TVIVTGANTGIGKQTALRLARGGNIIACRDMEKCEAAKDIRGETLNHHVNAHLDLA 99
 DB 35 TAITGTGTGIGMETARVLKRGAVVIGARNMGAAENAKTEILRONANARVLTLLQDL 94
 QY 100 SLKSIREFAAKIIEEERVDILI-----NNAGVMRCPHWTTEDGFE 140
 DB 95 SIKSIKAFVREFHALHLPENLLMYTSLSIQKAFAPPLANNAGWFCFYQLSEDCIE 154
 QY 141 MQFGVNHGFLHFLTNLLDLKLKASAPS-----RIINLSLAHVAGH-----IDFDLWQTKR 192
 DB 155 LQFATNHHGFLTNLLDLMKNTAKTSVGVEGRILNVSSVAHVITYQEGIQFQDSIN-DIC 213

QY 136 EDGFMFGVNHGHLFTLNLLDKLKASAPSR:INLSSLAHVAGHIDFDLNMQTRKYN 195
 Db 113 ADGPELOFGSNHGHFALTAHLPLRAAQRVSVLSLSLAARRGRHFDLDQFE-RSYA 171
 QY 196 TKAAYCQSKLAIVLFTKELSRLO--QSGVTVNALHPCVARTELGRHTGTHGST- 247
 Db 172 PMTAYGQSKLAVLPARELDRSRAAGWIIISNAHPGLTKTNQIAGSPHGRDKPALME 231
 QY 248 ---FSSSTLTGPIFWLLVKSPELAQPSSTYLAABELADVSGKYF-----DGLKQ- 293
 Db 232 RLYKTSWFAFLPQOEIEEGIL--FALY-AAATPQAD-GGAFYGRGRVAVGGGVREA 286
 QY 294 KAPAPAEDEEVARLWAEARLVGLEAPSVR 325
 Db 287 KVPAAARNAD-SKRLWEVSEQLTGVSYPKSR 317

RESULT 11
 D84206
 probable oxidoreductase [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: D84206
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Junc, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: D84206
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-316 <STO>
 A:Cross-references: GB:AE004437; NID:g10580084; PIDN:AAG19016.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: YajO1
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.0%; Score 457.5; DB 2; Length 316;
 Best Local Similarity 38.6%; Pred. No. 6.4e-29;
 Matches 120; Conservative 43; Mismatches 129; Indels 19; Gaps 8;

QY 23 DYVTGACPSKATIPKTVITGANTGIGKOTALELARRGGNIILACRDMKECEAAAKDI 82
 Db 5 DAWTAALPDQS---GRRVVVTGANSGLGFETAPAFAGAHVVMACRSTERGEDARDI 61
 QY 83 RGETLNHNHVARHLDLASKSIREFAKIIIEEERVDILINNAGVRCPHWTTEDGPEMQ 142
 Db 62 VAEPLGASLTVHDLDAALDSVAADFADWFTAEFDSLHVANNAGVMAIPRSTADGFETQ 121
 QY 143 FGVNHLGHFLLTNLLDKL-KASAPSR:INLSSLAHVAGHIDFDLNMQTRKYNKAAVC 201
 Db 122 FGVNHLGHVALTAGLLGLVLRRTSGETRVVTQSSGAHRRGRIDFEDLQHEA-EYKWEAYS 180
 QY 202 QSKLAIVLFTKELSRLOQSGVTVN--ALHPGVARTELG-RHTGTHGSTTIGPFW 258
 Db 181 QSKLANLLFAYELDRLELRASASVTSVACHPGVATNLQIRGPQAQSLRLILARAANA 240
 QY 259 LLVKSPELAQPSSTYLAABELADVSGKYF--DGL-----KQKAPAEAEDEEVARLL 309
 Db 241 LVQQSREOQAWFLLYAATNPSID--GGEYIGPGVLNMGHPRQPSARSDEDTAREL 298
 QY 310 WAESARLVGLE 320
 Db 299 WTVSADRTGVD 309

RESULT 12
 T10561
 hypothetical protein F25E4.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 04-Mar-2000
 C:Accession: T10561
 R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16533
 A:Accession: T10561
 A:Molecule type: DNA
 A:Residues: 1-317 <REV>
 A:Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.30
 A:Experimental source: cultivar Columbia; BAC clone F25E4
 C:Genetics:
 A:Gene: ATSP:F25E4.30
 A:Map position: 4
 A:Introns: 36/1; 113/2; 140/1; 191/2; 217/3; 246/1; 261/3
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.9%; Score 456; DB 2; Length 317;
 Best Local Similarity 37.2%; Pred. No. 8.4e-29;
 Matches 109; Conservative 56; Mismatches 112; Indels 16; Gaps 5;

QY 38 GKTIVITGANTGIGKOTALELARRGGNIILACRDMKECEAAAKDIRETINHNHVARHLD 97
 Db 29 GLTAIVTGASSGIGETTRVLAIRGVHVMAYVNTDSGNQVRDKILKEIPQAKIDVWKLD 88
 QY 98 LASLKSIREFAKIIIEEERVDILINNAGVRCPHWTTEDGFMQGVNHLGHFLLTNLL 157
 Db 89 LSSMASVRFSFSEYQSLDLPMLLNNAGIMACPFLLSSDNIELOFATNHLGHFLLTNLL 148
 QY 158 LDKLKASA-----PSRIINLSSLAHVAGH---IDFDLNMQTRKYNKAAVCQSKLAIVL 209
 Db 149 LERMKKTASESNREGRIIVVSSECHRFAYREGVQFKINDEAR-YNTLQAYGQSKLGNIL 207
 QY 210 FTKELSR--RLQSGVTVNALHPCVARTELGRHTGTHGSTTIGPFWLLVKSPELA 267
 Db 208 HATELARLPKEQGVNTANSLSHPGSIWNTLLRY-----HSFINTIGNAVGKYLVKSIPOG 262
 QY 268 AQSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARLWAEARLVGLE 320
 Db 263 AATTCYAALHPQAKGVSGEYIMDNNDSPNSQGGKDKLAKKLWFEFLRLTGE 315

RESULT 13
 C83017
 Probable short chain dehydrogenase PA5031 [imported] - Pseudomonas aeruginosa (strain P
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: C83017
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: C83017
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-309 <STO>
 A:Cross-references: GB:AE004916; GB:AE004091; NID:g9951315; PIDN:AAG08416.1; GSPDB:GN00
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA5031
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.6%; Score 451; DB 2; Length 309;
 Best Local Similarity 39.2%; Pred. No. 2e-28;
 Matches 121; Conservative 37; Mismatches 121; Indels 30; Gaps 9;

QY 32 SKATIP---GKTIVITGANTGIGKOTALELARRGGNIILACRDMKECEAAAKDIRETIN 88
 Db 5 TRRNIPQAGRLLAVTGANSGLGWQAARTLAGKATVVMACRNEQEARARRALLDEYPQ 64
 QY 89 HHVVARHLDLASKSIREFAKIIIEEERVDILINNAGVRCPHWTTEDGFMQGVNHL 148

Db 65 ARLEADLDLADLASIRACAGFRQHRARLDLFFNAGVMFLPLRRTRDGFEMQGTNHL 124
QY 149 GHFLTLNLLDKLKASAPSIINLSLAHVAGHIDFDLNNWOTRKNTKAAVCSQSLATV 208
Db 125 GHFALTGLDLSLAAPRPVGTGFGFGLPDLDDNAE--RGNRYLAIVCHSQANL 183
QY 209 LFTKESRRRQSGGVTVNAL--HPGVARTELGRHTGHGTSFTSTTLGPIFWLL----- 260
Db 184 LFSLELQRRAGQGVLLQSLAHPGVAAATNL-----QVAAPAMSGSRLGR--WAMKVANGA 237
QY 261 -VKSPELAAPSTYLAVAELADVSGKYFD-----GLKQKAPAP-EAEDEEVARRLW 310
Db 238 FASAEAGMALPA--LSALTEQRVGGAYGPDRLWLETRGYPAAARIPRNARDUGLAARUW 295
QY 311 AESARLVGL 319
Db 296 ALSEELGV 304

RESULT 14
T13447
hypothetical protein T19F6.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Mar-2000
C:Accession: T13447; T13449
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17587
A:Accession: T13447
A:Molecule type: DNA
A:Residues: 1-332 <BBV>
A:Cross-references: EMBL:AL109619; GSPDB:GN00062; ATSP:T19F6.40
A:Experimental source: cultivar Columbia; BAC clone T19F6
C:Genetics:
A:Gene: ATSP:T19F6.40
A:Map position: 4
A:Introns: 41/1; 118/2; 145/1; 197/2; 224/3; 254/1; 269/3
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.4%; Score 447.5; DB 2; Length 332;
Best Local Similarity 40.3%; Pred. No. 4.3e-28;
Matches 118; Conservative 47; Mismatches 105; Indels 23; Gaps 9;

QY 40 TVIVTGANTGIGKQTALEARGGNIILACRDMKCEAAAKDIRGETLNHHVNRHLDLA 99
Db 36 TAVITGATGIGASTARVIAKRGARLIFPARNVKAAEAKERIVSEPPETEIIVVMKIDLS 95
QY 100 SLKSIRPEAAKIIIEEERVDILINNAGVMRCPHPTTDDGFEMQGVNHLGHFLTLNLLD 159
Db 96 SIASVRNPFADPFESLDLPLNLLINNAGKLAHEHAISEDGIEMTFATNYLGHFLTLNLLN 155
QY 160 KL-----KASAPSIINLSLAH--VAGH-IDFDLNNWOTR-KYNTKAAVCSQSLAIVLF 210
Db 156 KWIQTAEETGVQGRIVNVTSIGIHGWFSGDLIEYLRLLISQPKQPDATRAVALSKLANVLH 215
QY 211 TKELSRRLQ--GSGVTVNALHPGVARTELGR-HTGINGHSFTSTTLGPIFWL---LVKSP 264
Db 216 TKELSSRLQKIGAMVTVCNHPGVYRTLTLDREGL-----LFDL--VFFLASKLVKTV 267
QY 265 ELAQPSTYLAVAELADVSGKYFDGLKQKAPAPAEDEEVARRLWAESARLV 317
Db 268 PQRAATTCYATNPRLVNVSQKYTFDCNETTPSGLTGINSSEATKLAASEILV 320

RESULT 15
AE3195
dehydrogenase Atu5290 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AE3195
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, D.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:111743193
A:Accession: AE3195
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <KUR>
A:Cross-references: GB:AB008687; PIDN:AAL45979.1; PID:g17743732; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu5290
A:Genome: plasmid
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.9%; Score 438.5; DB 2; Length 301;
Best Local Similarity 38.2%; Pred. No. 2e-27;
Matches 117; Conservative 52; Mismatches 110; Indels 27; Gaps 11;

QY 32 SKATIP---GKTIVTGANTGIGKQTALEARGGNIILACRDMKCEAAAKDIRGETLN 88
Db 5 TEANIPNQRGRSAVVVTGTG-GLGLETALALARAGCDVTIAGRNPKEGSDAVSRIORAAPH 63
QY 89 HHVNARHLDLASLSIREFAAKIIIEEERVDILINNAGVMRCP-HWTTEDFEMQGVNHH 147
Db 64 VTVSEKLDLADLSIALFAQEMENDRESLDLLVNNAGIMVPPKXQETRDGFELQFGTNY 123
QY 148 LGHFLTLNLLDKLKASAPSIINLSLAHVAGHIDFDLNNWOTRKNTKAAVCSQSLAI 207
Db 124 LGHFALTALHMLPKKGTDRVTVSVVAARAGKINFADIN-SEKNYHPMRYAQSKLAC 182
QY 208 VLFTKELS--RLQSGVTVNALHPGVARTELGRHTGHGTSFTSTTLG---PIFWLILVK 262
Db 183 LMFALLEQDRSRAGAGWGVSSIAHPGVSRITDL-----LHNAPGRNSLQGLARTFLWFLFQ 237
QY 263 SPELAQPSTYLAVAELADVSGKYF--DGLKQ-----KAPA---PEAEDEEVARRLWAES 313
Db 238 PVAQCALPQLFSATSKYVK--SGGYGPDRLGTRGHGPQPARIPPEALDRVAGKQLWEIS 295
QY 314 ARLVGL 319
Db 296 QMTGL 301

Search completed: June 23, 2004, 11:09:00
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2004, 11:03:04 ; Search time 17 Seconds
(without alignments)
1013.837 Million cell updates/sec

Title: US-10-015-393A-116

Perfect score: 1695

Sequence: 1 MSRYLLPLSALGTAGAAVL.....ESARLVGLEAPSVREQLPLR 331

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	99.6	331	1	RDHD_HUMAN
2	1443.5	85.2	334	1	RDHD_MOUSE
3	739.5	43.6	318	1	RDHB_HUMAN
4	738.5	43.6	316	1	RDHC_MOUSE
5	737.5	43.5	316	1	RDHB_HUMAN
6	730.5	43.1	316	1	RDHB_MOUSE
7	726	42.8	336	1	RDHE_HUMAN
8	722.5	42.6	334	1	RDHE_MOUSE
9	714	42.1	316	1	RDHC_BOVIN
10	532	31.4	330	1	DRSX_HUMAN
11	408.5	24.1	280	1	DRSX_MOUSE
12	364.5	21.5	398	1	POR_DAUCA
13	356	21.0	397	1	POR_CHLRE
14	353.5	20.9	298	1	OXIR_STRLT
15	352	20.8	297	1	OXIR_STRLI
16	346.5	20.4	405	1	PORA_ARATH
17	345.5	20.4	399	1	POR_PEA
18	342	20.2	388	1	PORA_HORVU
19	339	20.0	388	1	PORA_WHEAT
20	338.5	20.0	401	1	PORA_ARATH
21	338	19.9	398	1	PORA_CUCSA
22	336	19.8	322	1	POR_PLEBO
23	331	19.5	313	1	POR_AVEA
24	329	19.4	401	1	PORC_ARATH
25	326.5	19.3	395	1	PORB_HORVU
26	325	19.2	322	1	POR_SINY3
27	310.5	18.3	458	1	POR_MARPA
28	289	17.1	407	1	YNS1_YEAST
29	242.5	14.3	267	1	YMS1_YEAST
30	237.5	14.0	263	1	UCPA_SALTY
31	229.5	13.5	246	1	FABG_THEMA
32	222.5	13.1	263	1	UCPA_ECO57
33	222.5	13.1	263	1	UCPA_ECOLI

34 222 13.1 272 1 DHK1_STRVN P16542 streptomyc
35 218.5 12.9 246 1 FABG_BACSU P51831 bacillus su
36 218.5 12.9 592 1 EPHD_MYCTU Q10402 mycobacteri
37 215 12.7 247 1 FAGI_SYNY3 P73574 synechocyst
38 214 12.6 241 1 FABG_RICPR P50941 rickettsia
39 214 12.6 248 1 FABG_AQUAB O67610 aquifex aso
40 213.5 12.6 251 1 Y325_THEMA Q9WY60 thermotoga
41 212 12.5 412 1 BL14_NEUCR Q92247 neurospora
42 210 12.4 320 1 FABG_CUPLA P28643 cuphea lanc
43 207 12.2 281 1 YL46_BRAJA Q45219 bradyrhizob
44 205 12.1 256 1 RHLG_PSEAE Q95101 pseudomonas
45 204 12.0 244 1 FABG_VIBCH Q9K977 vibrio chol

ALIGNMENTS

RESULT 1
RDHD_HUMAN STANDARD; PRT; 331 AA.
ID RDHD_HUMAN STANDARD; PRT; 331 AA.
AC Q8NB7; 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Retinol dehydrogenase 13 (EC 1.1.1.-).
GN RDH13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=teratocarcinoma;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP TISSUE SPECIFICITY, AND ENZYMOLOGICAL ACTIVITY.
RX MEDLINE=223226; PubMed=1226107;
RA Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,
RA Matsumura M., Nelson P.S., Palczewski K.;
RT "Dual-substrate specificity short chain retinol dehydrogenases from
the vertebrate retina."
RL J. Biol. Chem. 277:45537-45546(2002).
CC -I- FUNCTION: Does not exhibit retinol dehydrogenase (RDH) activity in
vitro.
CC -I- TISSUE SPECIFICITY: Expressed mostly in eye, pancreas, placenta
and lung in the retina, detected in the inner segment of the
photoreceptor cells. Weak signals were observed in a small
population of inner nuclear neurons and the inner plexiform layer.
CC -I- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AK075392; BAC11591.1; -
CC Genew; HGNC.19978; RDH13.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
FT Oxidoreductase; NADP.
FT NP BIND 45 51 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 200 200 BY SIMILARITY.
FT ACT SITE 331 AA; 35902 MW; E84A3759DD2D274F5 CRC64;
SQ SEQUENCE

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Prostate;
RX MEDLINE=21139103; PubMed=11245473;
RA Lin B., White J.T., Ferguson C., Wang S., Vessella R., Bumgarner R.,
RA True L.D., Hood L., Nelson P.S.;
RT "Prostate short-chain dehydrogenase reductase 1 (PSDR1): a new member
RT of the short-chain steroid dehydrogenase/reductase family highly
RT expressed in normal and neoplastic prostate epithelium.";
RL Cancer Res. 61:1611-1618 (2001).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Liver;
RA Li X., Wang L., Cheng J., Zhang L., Lu Y., Liu Y., Duan H.;
RT "Screening of HCV core binding protein from human liver cDNA library
RT by using yeast two hybrid system.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=20272150; PubMed=10810093;
RX Lai C.-H., Chou C.-Y., Chang L.-Y., Liu C.-S., Lin W.-C.;
RA "Identification of novel human genes evolutionarily conserved in
RA Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713 (2000).
[4]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Brain, Muscle, Placenta, and Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S., Krzyzanski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[5]
IDENTIFICATION AS A RETINAL REDUCTASE, AND SUBCELLULAR LOCATION.
RX MEDLINE=22151122; PubMed=12036956;
RA Kedishvili N.Y., Chumakova O.V., Chetyrkin S.V., Belyaeva O.V.,
RA Lashina E.A., Lin D.W., Matsumura M., Nelson P.S.;
RT "Evidence that the human gene for prostate short-chain
RT dehydrogenase/reductase (PSDR1) encodes a novel retinal reductase
RT (Rair1).";
RL J. Biol. Chem. 277:28909-28915 (2002).
CC -!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
CC retinoids. Most efficient as an NADPH-dependent retinal reductase.
CC Displays high activity toward 9-cis and all-trans-retinol. Also
CC involved in the metabolism of short-chain aldehydes. No steroid
CC dehydrogenase activity detected.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC Associated with endoplasmic reticulum membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8TC12-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8TC12-2; Sequence=VSP_008159;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Predominantly expressed in the epithelial

cells of prostate, in both basal and luminal secretory cell
populations. Expressed at low levels in spleen, thymus, testis,
ovary, small intestine, colon, peripheral blood leukocytes,
kidney, adrenal gland and fetal liver. Not detected in prostatic
fibromuscular stromal cells, endothelial cells, or infiltrating
lymphocytes.
CC -!- INDUCTION: By androgens, in prostate cancer cells.
CC -!- PTM: Not glycosylated.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF167438; AAF89632.1; -
CC EMBL; AF395068; AAK72049.1; -
CC EMBL; AF151840; AAD34077.1; -
CC EMBL; BC000112; AAH00112.1; -
CC EMBL; BC011727; AAH11727.1; -
CC EMBL; BC026274; AAH26274.1; -
CC EMBL; BC037302; AAH37302.1; -
CC EMBL; BC051291; AAH51291.1; -
CC Genew; HGNC:17964; RDH11.
CC MIM; 607849; -
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PROSITE; PRO0080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
CC Oxidoreductase; NADP; Signal-anchor; Transmembrane;
CC Endoplasmic reticulum; Alternative splicing.
CC TRANSMEM 1 21 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC CYTOPLASMIC (POTENTIAL).
CC NADP (BY SIMILARITY).
CC BY SIMILARITY.
CC Missing (in isoform 2).
CC /FTId=VSP_008159.
CC
CC CONFLICT 176 176 S -> F (IN REF. 4; AAH51291).
CC CONFLICT 294 294 A -> V (IN REF. 1).
CC CONFLICT 316 316 P -> S (IN REF. 4; AAH26274).
CC
CC SEQUENCE 318 AA; 35386 MW; 5B0C366552774835 CRC64;
SQ
Query Match 43.6%; Score 739.5; DB 1; Length 318;
Best Local Similarity 50.7%; Pred. No. 5.9e-53;
Matches 155; Conservative 49; Mismatches 89; Indels 13; Gaps 3;
QY 17 AAVLLKDYVTGGACPSKATIPGKTVIVTGTANTGIGKQTALRLARGGNIILACRDMKCE 76
Db 20 AAAPQIKMLSSGCVCTSTVQLPGKVVVVVTGANTGIGKETAKELAQARGVYLACRDVKEGE 79
QY 77 AAADIRIGBTLLNHNHNAHDLASLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTE 136
Db 80 LVAKELIQTITGNOQVIVRKLDLSDTKSIRAFKGLAEKHLVLINNAGVMRCPSKTA 139
QY 137 DGFENQFGVNHGHFLNLLLDKLIKASAPRIINLSSLAHVAGHIDDDLLNMQTRKNT 196
Db 140 DGFEMHIGVNHGHFLNLLLEKLEKESAPRIVNVSSLAHLGLRIHFHNLQGE-KFYNA 198
QY 197 KAAVCOSKLAIVLFTKELSRRLQSGVTVNHLPGVARTELGRHTGIHGTSFSSITLGP 256
Db 199 GLAYCHSKLANILFTQELARLKGSGVTYSVHPGTVQSELVRH-----SFMWM 249
QY 257 FWL---LVKSPELAAQPSITYLAVASELADVSGKYFDGLKQKAPAEAEDEEVARLEWAE 313
Db 250 WWLFSFFIKTPQOGAQTSLHCALTGLEILTSNGHFSDCHEVAVMSAQARNETIARELWDVS 309
QY 314 ARLVGL 319
|:|

Db 310 CDLLGL 315

RESULT 4

RDHC MOUSE

ID RDHC MOUSE STANDARD; PRT; 316 AA.

AC QBYK4; Q91WA5; Q9D1Y4;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Retinol dehydrogenase 12 (EC 1.1.1.-).

GN RDH12.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [!]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Spinal cord;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kakukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tonaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilmig L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs";

RL Nature 420:563-573(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Retina;

RX MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield F.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards

CC retinoids. Most efficient as an NADPH-dependent retinal reductase.

CC Displays high activity toward 9-cis and all-trans-retinol. Also

CC involved in the metabolism of short-chain aldehydes. No steroid

CC dehydrogenase activity detected. Might be the key enzyme in the

CC formation of 11-cis-retinal from 11-cis-retinol during

CC regeneration of the cone visual pigments (By similarity).

CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

CC (SDR) family.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AK020927; BAB32258.1; -

DR EMBL; AK039233; BAC30288.1; -

DR EMBL; BC016204; AAH16204.1; -

DR MGD; MGI:1925224; Rdh12.

DR InterPro; IPR002198; ADH short.

DR Pfam; PF00106; adh_short7.1.

DR PRINIS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; FALSE_NEG.

DR Oxidoreductase; NADP; Vision.

KW NP BIND 46 52 NADP (BY SIMILARITY).

FT ACT SITE 200 200 BY SIMILARITY.

FT CONFLICT 114 125 MISSING (IN REF. 2).

FT CONFLICT 120 120 H -> D (IN REF. 1; BAB32258).

FT SEQUENCE 316 AA; 35292 MW; CF5745B6710A6148 CRC64;

QY Query Match 43.6%; Score 738.5; DB 1; Length 316;

Db Best Local Similarity 48.7%; Pred. No. 7.1e-53;

QY 5 LILPSALGTWAGAAVLKDYVYGACPSKATIPGKTVITVGANTGIGKOTALELARGGN 64

Db 6 VLLTSFSLYLTAPSKPPFAGGVCTNVQIPKVVITGANTGIGKOTALELARGAR 65

QY 65 IILACRDMKECAAAKQIRGTNLNHHVNHARHLDIASLKSIRFPAKIIIEBERVDILNN 124

Db 66 VVIACRDVLKGEAAASEIRADTKNSQVLVRKLDLSDTKSIKIRAFERFLASEKHLILNN 125

QY 125 AGVRCCHWTTEDEGFMQGVNHLGHLLTLLDLDLKLKASAPSIINLSIAHVAGHIDF 184

Db 126 AGVMMCPYSKTTDGFETHFGVNHGHLLTLLDLDLKLKASAPSIINLSIAHVAGHIDF 185

QY 185 DDLNMQTRKYNKTAAYCQSKLAIVLFTKLSRRLOQSGVTVNALHPGVARTELGRHTGIH 244

Db 186 HDLQSQ-KRYCSAFAYGHSKLANLFTRELAKRLQGTAYAVHPGVVLSEITR- 239

QY 245 GSTFSSTLIGIFWLLVKSPELAQPSYTLAVABELADVSKYFDGLKQKAPAEADEE 304

Db 240 -NSVLLCLLWLFSPFFKSTSQGAQTSIHLCALADEPLSGKPSFDCRMVSSRRNKK 298

QY 305 VARRLWAEASRLVGLIE 320

Db 299 TAERLWNVSCELGIGI 314

RESULT 5

RDHC HUMAN

ID RDHC HUMAN STANDARD; PRT; 316 AA.

AC Q96NR8; Q8TAM6;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Retinol dehydrogenase 12 (EC 1.1.1.-).

GN RDH12.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA Sugiyama T., Irie R., Osuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RT "NEO human cDNA sequencing project";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP FUNCTION.
RX MEDLINE=22323226; PubMed=12226107;
RA Haeseleer F., Jiang G.-F., Tmanishi Y., Driessen C.A.G.G.,
RA Matsumura M., Nelson P.S., Palczewski K.,
RT "Dual-substrate specificity short chain retinol dehydrogenases from
the vertebrate retina.";
RL J. Biol. Chem. 277:45537-45546 (2002).
CC -!- FUNCTION: Exhibits an oxidoreductase catalytic activity towards
retinoids. Most efficient as an NADPH-dependent retinal reductase.
CC Displays high activity toward 9-cis and all-trans-retinol. Also
CC involved in the metabolism of short-chain aldehydes. No steroid
CC dehydrogenase activity detected. Might be the key enzyme in the
CC formation of 11-cis-retinal from 11-cis-retinol during
CC regeneration of the cone visual pigments.
CC -!- TISSUE SPECIFICITY: Widely expressed, mostly in eye, kidney,
CC brain, skeletal muscle and stomach.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
CC
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CC or send an email to license@isb-sib.ch).
CC
CC
CC EMBL; AK054835; BAB70811.1; --
CC EMBL; BC025724; AAB75724.1; --
CC GenBank; HGNC:19977; RDB12.
CC InterPro: IPR002198; ADH short.
CC Pfam: PF00106; adh short_1.
CC PRINTS; PR0080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; FALSE_NEG.

KW Oxidoreductase; NADP; Vision.
FT NP BIND 46 52 NADP (BY SIMILARITY).
FT ACT SITE 200 BY SIMILARITY.
FT CONFLICT 161 Q -> R (IN REF. 1).
SQ SEQUENCE 316 AA; 35065 MW; EA0B8CFF99B67A8 CRC64;

Query Match 43.5%; Score 737.5; DB 1; Length 316;
Best Local Similarity 50.3%; Pred. No. 8.6e-53;
Matches 151; Conservative 49; Mismatches 92; Indels 7; Gaps 2;

QY 21 LKDYVYTGAGCPKATIPGKTVITGANTGIGQTALEARRGNIIILACRMEKCEAAAK 80
DB 22 IRKFFAGGVCRNTVQPLGKVVITGANTGIGKETAELASRGARVVIACRDLVKGSAAS 81
QY 81 DIRGETLNHHVNAHIDLASLSIREFAAKITEEERVDILINAGVMCPHWTTEDGEE 140
DB 82 EIRVDTKNSQVLVKLDLSDTKSIRAFAGFLAEKQHLILNNAVMCPYSKTADGFE 141
QY 141 MQGVNHLGHFLTLNLLDKLAKASAPRIINSLAHVAGHIDFDLNNQTKRYNTKAY 200
DB 142 THLVGNHLGHFLTLNLLQKVSAPRVNVSSVAHIGKIPFHDQ-SEKYSRGPAY 200
QY 201 CQSKLAIVFTKELSRRLQSGVTVNALHPGVARTLGHRTGHSTFSTILGPIFWLL 250
DB 201 CHSKLANVLFRELAERLQGTGTVTVYHVGVRSELVHSSD-----LCLLWRLFSPF 254
QY 261 VKSPFELAAQSTYLAVALAEELADVSGYFDGLKQKAPAEAEDEVARRLWAESARLVGL 319
DB 255 VKTAREGAQTSLHCAEAEGLEPLSGKFSCKETWSPRANNNKTAERLWNVSCCELLGI 313

RESULT 6
RDHB MOUSE
ID RDHB_MOUSE STANDARD; PRT; 316 AA.
AC QSQVEI; QSDQUS;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (Rall1)
DE (Prostate short-chain dehydrogenase/reductase 1) (Androgen-regulated
DE short-chain dehydrogenase/reductase 1) (Short-chain aldehyde
DE dehydrogenase) (SCALD) (Cell line MC/9.IL4 derived protein 1)
DE (M42C60)
DN RH11 OR PSDR1 OR ARSDR1 OR MDT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Mast cells;
RX MEDLINE=94289700; PubMed=8018917;
RA Hara T., Harada N., Mitsui H., Miura T., Ishizaka T., Miyajima A.;
RT "Characterization of cell phenotype by a novel cDNA library
RT subtraction system: expression of CD8a in a mast cell-derived
RT interleukin-4-dependent cell line.";
RL Blood 84:189-199 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22133316; PubMed=12137953;
RA Moore S., Pritchard C., Lin B., Ferguson C., Nelson P.S.;
RT "Isolation and characterization of the murine prostate short-chain
RT dehydrogenase/reductase 1 (Psd1) gene, a new member of the
RT short-chain steroid dehydrogenase/reductase family.";
RL Gene 293:149-160 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22803395; PubMed=12807874;
RA Kasus-Jacobi A., Ou J., Bashmakov Y.K., Shelton J.M., Richardson J.A.,
RA Goldstein J.L., Brown M.S.;
RT "Characterization of mouse short-chain aldehyde dehydrogenase
RT (SCALD), an enzyme regulated by SREBFs.";

J. Biol. Chem. 0:0-0(2003).

[4]

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=22354683; PubMed=12466851;
OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Gough J.,
Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teatou M., Tomita M.,
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Shiraki T., Waki K., Kawai J., Azawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imotani K., Ienli Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
Nature 420:563-573 (2002).

[5]

SEQUENCE FROM N.A.

TISSUE=Breast tumor;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McWeney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
retinoids. Most efficient as an NADPH-dependent all-trans-retinal
reductase. Also involved in the metabolism of short-chain
aldehydes.

-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).

-!- ASSOCIATED WITH: endoplasmic reticulum membrane (By similarity).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced;

Name=1;

-!- TISSUE SPECIFICITY: Expressed at higher level in liver and testis.
Expressed at lower levels in smooth muscle, thymus, submaxillary
gland and epididymis. In testis, expression is restricted to the
pachytene spermatocytes. Also expressed in four layers of the

retina, including the outer segment of rods and cones.

-!- PTM: Not glycosylated (By similarity).

-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.

-!- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 311.

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or send an email to license@isb-sib.ch.

EMBL; AB035959; BAA88521.1; ALT_FRAME.
EMBL; AV039032; AAK91516.1; -
EMBL; AF474027; AAL79910.1; -
EMBL; AK004413; BAE23296.1; -
EMBL; BC018261; AAH18261.1; -
MGD; MGI:102581; Rdh11.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00080; SDRFAMILY.
PRINTS; PS00061; ADH_SHORT; FALSE NEG.
Oxidoreductase; NADP; Signal-anchor; Transmembrane;
Endoplasmic reticulum; Alternative splicing
TRANSMEM 1 21 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
DOMAIN 22 316 CYTOPLASMIC (POTENTIAL).
ACT SITE 199 199 BY SIMILARITY.
NP_BIND 45 51 NADP (BY SIMILARITY).
CONFLICT 238 238 R -> G (IN REF. 1).
CONFLICT 279 279 S -> R (IN REF. 1).
SEQUENCE 316 AA; 35148 MW; 62FAE25585CC05FE CRC64;

Query Match 43.1%; Score 730.5; DB 1; Length 316;
Best Local Similarity 50.2%; Pred. No. 3.2e-52;
Matches 150; Conservative 50; Mismatches 92; Indels 7; Gaps 2;

QY 21 LKDYVTGACPSKATIPGKTIVIVTGANTGKQTALEALRGGNIILACRDMKECAAAK 80
::: ::::SSGVCYSNVQLFGKVAIVTGANTGIGETAKDLAQRGAVYLACHDVKGLAAR 80
Db 21 IRKMLSSGVCYSNVQLFGKVAIVTGANTGIGETAKDLAQRGAVYLACHDVKGLAAR 80
QY 81 DIRGTLNHHVNAHRLDLASLKSITREPAKIIIEERVDILINNAGVMRCPHWTTEGFE 140
::: ::::SSGVCYSNVQLFGKVAIVTGANTGIGETAKDLAQRGAVYLACHDVKGLAAR 140
Db 81 EIQAVTGNQSQVFRKDLADTKSTRAPAKDFLAEEKHLHLINNAGVMRCPHWTTEGFE 140
QY 141 MFGVNHGLGHLLTLNLDKDKADAPSRINLSSLAHVAGHIDPDDLNWQTKNTKAA 200
141 MHGIVNHGLGHLLTLNLDKDKADAPSRINLSSLAHVAGHIDPDDLNWQTKNTKAA 200
Db 141 MHGIVNHGLGHLLTLNLDKDKADAPSRINLSSLAHVAGHIDPDDLNWQTKNTKAA 200
QY 201 COSKLAIVLFKELSRRLQSGVTVNALHPQVAETELGRHTGHGTSFTTLTGPIFWLL 260
::: ::::SSGVCYSNVQLFGKVAIVTGANTGIGETAKDLAQRGAVYLACHDVKGLAAR 260
Db 200 CHSKLANLFTFKELAKLKGSGVTYSVHPGTVHSELTTRYSSI-----MRWLQLEFFV 253
QY 261 VKSPLELAQPSYLAVALAEADVSGKVPDGLKQKAPAEAEDEEVARRLWAESARLVGL 319
::: ::::SSGVCYSNVQLFGKVAIVTGANTGIGETAKDLAQRGAVYLACHDVKGLAAR 319
Db 254 IKTPOEGATSLYCALTEGLESLSGHFSDCQLAWSVQGRNEIILARRLMDVSCDLLGL 312

RESULT 7

ID RDHE HUMAN STANDARD; PRT; 336 AA.

AC Q9BHS5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Retinol dehydrogenase 14 (EC 1.1.1.-) (Alcohol dehydrogenase PAN2).

GN RDH14 OR PAN2.

OS Homo sapiens (Human).

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RT "pan2, a novel member of the SCAD superfamily.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3];
RP FUNCTION.
RX MEDLINE=2232226; PubMed=12226107;
RA Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,
RA Matsumura M., Nelson P.S., Palczewski K.;
RT "Dual-substrate specificity short chain retinol dehydrogenases from
RL the vertebrate retina.";
RL J. Biol. Chem. 277:45337-45546(2002).
CC -1- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
CC retinoids. Most efficient as an NADPH-dependent retinal reductase.
CC Displays high activity toward 9-cis and all-trans-retinol. No
CC steroid dehydrogenase activity detected.
CC -1- TISSUE SPECIFICITY: Expressed in brain, kidney, pancreas and
CC Placenta.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF237952; AAG12190.1; -
DR EMBL; BC009830; AA09830.1; -
DR HSP; PS0162; IAE1.
DR HSP; HGNC:19979; RDH14.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
KW Oxidoreductase; NADP.
FT ACT_SITE 217 217 BY SIMILARITY.
FT NP_BIND 50 56 NADP (BY SIMILARITY).
SQ SEQUENCE 336 AA; 36864 MW; BCC17B3CD6B70DED CRC64;
Query Match 42.8%; Score 726; DB 1; Length 336;
Best Local Similarity 50.0%; Pred. No. 8e-52;
Matches 150; Conservative 44; Mismatches 80; Indels 26; Gaps 4;

```

```

QY 38 KTVIVTGTANTGIGKQTALRLARRGGNIILACDMKCEAAAKDIR----- 83
DB 43 GKTVLITGANSGLGRATAAEELLRLGARVINGCDRAEEAAGQLRRLRQAACGPEPG 102
QY 84 ---GETLNHHVNARHLDLASLSKISREFAAKIIIEEERVDILINNAWMCPCPHWTEDGF 139
DB 103 VSGVGELI-----VRELDLASLSRAVAFQCEMLQEPRLDLVNNAGIFQCPYMKTEDGF 157
QY 140 EMQFGVNHGHFLITLNLIDKLKASAPSRININSLAHVAGHIDFDLNNQTRKYNITKAA 199
DB 158 EMQFGVNHGHFLITLNLIDKLKSSAPSRIVVSSKLYKYGDINFDLNL-SEOSYNKSF 216
QY 200 YCQSKLAIVLFTKELSRRLQSGVTNNALHPGVARTLGRHTGHGTSFTSTLGPFWL 259
DB 217 YSRSKLANILFTRELARLSTNTVNVVLPHGIVRTNLGRH--IHIFLLVKPLFNLVSWA 274
QY 260 LVKSPLELAOPSTVLAELADVSGKYFDGLQKQAPAPAEDEEVARRLWASARLVGL 319
DB 275 PFKTPVEGAQTSITYLASSPEVSGRYFGDCKEELLPRAMDESVARKLWDISEVMVGL 334

RESULT 8
RDHE_MOUSE STANDARD; PRT; 334 AA.
AC Q9ERI6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Retinol dehydrogenase 14 (EC 1.1.1.-) (Alcohol dehydrogenase PAN2).
GN RDH14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retal;
RA Li X.X., Breseton P.S., Obeyesekere V.R., Krowowski Z.S.;
RT "Cloning of the mouse Pan2 cDNA: a novel member of the short chain
RL alcohol dehydrogenase superfamily.";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
CC retinoids. Most efficient as an NADPH-dependent retinal reductase.
CC Displays high activity toward 9-cis and all-trans-retinol. No
CC steroid dehydrogenase activity detected (By similarity).
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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RA MEDLINE=21588066; PubMed=11731500;
 RA Gianfrancesco F., Sanges R., Esposito T., Tempesta S., Rao E.,
 RA Rappold G., Archidiacono N., Graves J.A.M., Forabosco A., D'Urso M.,
 RT "Differential divergence of three human pseudoautosomal genes and
 RT their mouse homologs: implications for sex chromosome evolution."
 RN Genome Res. 11:2095-2100(2001).
 RN [2]
 RN SEQUENCE FROM N.A., AND VARIANT LYS-297.
 RC TISSUE=Brain, Duodenum, and Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feilgenfeld E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max T.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RN SEQUENCE OF 127-330 FROM N.A.
 RP TISSUE=Testis;
 RC Koehnir K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- MISCELLANEOUS: Belongs to the pseudoautosomal region 1 (PAR1),
 CC located at the termini of the long and short arms of the X and Y
 CC chromosomes. This region is essential for meiotic pairing and
 CC recombination. Deletion of the PAR1 region causes male sterility.
 CC Genes in the PAR1 region escape X inactivation.
 CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 CC EMBL; AJ293620; CAC82170.1; -;
 DR EMBL; BC019696; AAH19696.1; ALT_INIT.
 DR EMBL; BC032340; AAH32340.1; -;
 DR EMBL; AL137300; CAB70685.1; -;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PS00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; Signal; Polymorphism.
 FT SIGNAL 1 31
 FT CHAIN 32 330
 FT -----
 FT DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER
 FT ON CHROMOSOME X.
 FT NP_BIND 47 71
 FT ACT_SITE 208 208
 FT VARIANT 297 297
 FT E -> K (in dbSNP:12010).
 FT /FTID=VAR_016100.
 FT CONFLICT 247 247 L -> V (IN REF. 2; AAH19696).
 FT SEQUENCE 330 AA; 36476 MW; 99F9EC7BC122911A CRC64;
 SQ
 Query Match 31.4%; Score 532; DB 1; Length 330;
 Best Local Similarity 40.3%; Pred. No. 5.2e-36;
 FT CHAIN 24 280
 FT SIGNAL 1 23
 FT CHAIN 24 280
 FT DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER
 FT ON CHROMOSOME X HOMOLOG.

Matches 133; Conservative 47; Mismatches 126; Indels 24; Gaps 8;
 QY 7 PLALGT-----VAGAAVLKDVY---TGAC-PSKATIPGKTVITGANTGIGKOTALE 57
 DB 3 PLGAARALRYAVAGRAVILAQLLRCRCGGFLFPVPPDRDVALVITGGTGGIGYSTAKH 62
 QY 58 LARRGNIIACRDMKCEAAKDIRGETLNHHVNHARHLDLASLKISIRFPAKIIIEER 117
 DB 63 LARLGMHVIAGNDSKAKQVSKIKEETLNDKVEFLYCDLAGMTSIRQVQFKMKKIP 122
 QY 118 VDLILNAGVMRCPHWTTEDGFMQGVNHLGHFLTLNLLDLKLKASA----PSRIINLS 173
 DB 123 LHVLINAGVMVQPKTRDGFEEHFGNLVGLHFLTLNLLDLTKESGSPHGARVVTVS 182
 QY 174 SLARVAGHIDFDLNLNMQTRKYNTKAAVCOSKLAIVLFTKLSRRL--QSGSVTVNALHPG 231
 DB 183 SATHYVAELNMDLIQ--SSACYSPPHAAVAQSKLAVLFTVHLORLLAAGSHVTANVVDPG 241
 QY 232 VARETLGRHGTGHGSPFSSFTLGP--IFWLLVKSPELAQPSYLAVAEELADVSGKYFD 289
 DB 242 VVNTDLVYK-----VFWATRLAKLGLWLLFTPDGAWTSIYAAVTPLEGVGGRIYLY 295
 QY 290 GLKQKAPAPAEDEEVARRLWAESARLVGL 319
 DB 296 NEXETKSLHTVYQKLLQQLWSKSCMTGV 325
 RESULT 11
 DHXS MOUSE
 ID DHXS MOUSE STANDARD; PRT; 280 AA.
 AC Q8VBZ0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dehydrogenase/reductase SDR family member on chromosome X homolog
 DE precursor (EC 1.1.1.-) (SCAD family protein) (DHRSX) (fragment).
 GN DHRSX OR PSCAD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Embryo;
 RX MEDLINE=21588066; PubMed=11731500;
 RA Gianfrancesco F., Sanges R., Esposito T., Tempesta S., Rao E.,
 RA Rappold G., Archidiacono N., Graves J.A.M., Forabosco A., D'Urso M.,
 RT "Differential divergence of three human pseudoautosomal genes and
 RT their mouse homologs: implications for sex chromosome evolution."
 RL Genome Res. 11:2095-2100(2001).
 CC -!- MISCELLANEOUS: Autosomal gene, which is the ortholog of human
 CC DHRSX, located at the termini of the long and short arms of the X
 CC and Y chromosomes.
 CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 CC EMBL; AJ296079; CAC82539.1; -;
 DR MGD; MGI:2181510; Dhxsx.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 280
 FT DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER
 FT ON CHROMOSOME X HOMOLOG.

DR	InterPro; IPR002198; ADH_short.
DR	InterPro; IPR005979; Frochl_reduct.
DR	Pfam; PF00106; adh_short; 1.
DR	TIGRFAMs; TIGR01289; LFOR; 1.
KW	Photosynthesis; Chlorophyll biosynthesis; Oxidoreductase; NADP;
KW	Chloroplast; Transit peptide.
FT	TRANSIT ? CHLOROPLAST (POTENTIAL).
FT	CHAIN ? 398 PROTOCHLOROPHYLLIDE REDUCTASE.
SQ	SEQUENCE 398 AA; 43365 MW; C81YD57FAVCF27D5 CRC64;
	Query Match 21.5%; Score 364.5; DB 1; Length 398;
	Best Local Similarity 34.4%; Pred. No. 3e-22;
	Matches 121; Conservative 48; Mismatches 134; Indels 49; Gaps 15;
QY	8 LSALGTVAGAAVLKDYTGCGACPSATTPGKTIVVTGANTCIGQTALELRBG-GNII 66 :
Db	55 ISQTGAIRSQAVATPPSWNRATGEKKTLRKGSVIITGASSGLGLATAKAETGKWHR 114 :
QY	67 LACDMEKCAAAKDTRGETLNHNHVARHLDIASLKSIREFAAKTIIEEERVDLIINAG 126 :
Db	115 MACRDFLKAERAKSACKPKNTI--MHLDDIASLDSVRQFVFETRSERLDLVLCNA 172 :
QY	127 V-----MRCPHTTWDGEMOGVNNHGFLTNLLDKL-KASAPS-RII----- 170 :
Db	173 VFPTAKEPTYA-DGFELSVGTNLGHFLSKLLLDLINKSDYSPKSLIIVSGITGN 231 :
QY	171 -----NLSIAHVAGIHDFDDLINQWT----RYNTKAAYCQSCLAIVLPTELRS 216 :
Db	232 TLAGNVPPKANGLDRLGAGCL--NGNSSAMIDGAFDGAKAYKDSKVCMLTWQEPFR 289 :

```

Db      290 RYHETGTTFASLVPFGCIATGTGFRE---HIPLF-RTLPPFPQKVIITKGYSVEAEGSKRL 345
QY      275 A--VAEELADVSGKYIFGLGKKAP-----APERAEDEVARRLWAESARLVGL 319
Db      346 AQWSEPSLTSGYGVSWNDKSASFENQLSEEASDYEKARKYWEVSEKLVL 397

RESULT 13
FOR_CHLRE
ID FOR_CHLRE STANDARD; PRT; 397 AA.
AC Q39617;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prochlorophyllide reductase, chloroplast precursor (EC 1.3.1.33)
DE [PCR] (NADPH-protochlorophyllide oxidoreductase) (POR).
GN POR OR LPCR-1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
NCBI TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L37C / CC-125;
RX MEDLINE=96197396; PubMed=8616232;
RA Li J., Timko M.P.;
RT "The pc-1 phenotype of Chlamydomonas reinhardtii results from a
RT deletion mutation in the nuclear gene for NADPH:protochlorophyllide
RT oxidoreductase."
RL Plant Mol. Biol. 30:15-37(1996).
CC -1- FUNCTION: Phototransformation of protochlorophyllide (Pchlide) to
CC chlorophyllide (Chlide).
CC -1- CATALYTIC ACTIVITY: Chlorophyllide A + NADP(+) =
CC protochlorophyllide + NADPH.
CC -1- PATHWAY: Chlorophyll biosynthesis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family. POR subfamily.
CC -----
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Matches	102;	Conservative	42;	Mismatches	128;	Indels	24;	Gaps	8;
Qy	36	IPGKTVITGANTGIGKQTAL	ELARRCGNIILACRDM	KECEAAAKDIRGETL	NHHYNARH	95			
Db	3	LTGRRVVTGGASGLGAETVR	ALAAAGAEVTIATRH	PQSAEPLVQAAAAAGAG	-RVHAEA	61			
Qy	96	LDLASLSIREFAAKIIEEER	VDILINNAGVRC	PHWT-TEDGFEMQFGVNH	LGHFLT	154			
Db	62	LDLSDVASVDSFAR---	AWRGPLDILVANAGI	NALPTRLTPYGNEMQLAT	NYLGHPALA	118			
Qy	155	NLLDLKLKASAPSR	IINLSSLAHVAGHID	FDLNNWQTRKYNTKAA	YQCSKLAIVLFTKEL	214			
Db	119	TGLHAALRDAGSARI	VVVSSCAHLGTDFED	PHFARRPYDPWAA	YGNSTADVLFTVG-	177			
Qy	215	SRRLQSGSVTVNALH	PGVARTLGRHTG----	IHGSTFSSTTLGP	IFWLLVKSPELAQ	269			
Db	178	ARRWAADGITANALN	PGYILTRLQRHVDD	ETMRAFGVMDQGNV	KPLFY--YKTPSQGAA	235			
Qy	270	PSTYLAVAEELADY	SGKYF-----	DG-LKQKAPAEAEDE	EVARELWAEASA	314			
Db	236	TSVLLAASPLNGVT	GRYFEDNQEAR	TVEDGDVQPGGVA	AHALDPEAADRLWEYGA	291			

Search completed: June 23, 2004, 11:08:27
Job time : 19 secs

QY 721 CTGAGCCGGCGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGGCTGGCC 780
Db |||||
1177 CTGAGCCGGCGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGGCTGGCC 1236
QY 781 AGGACAGAGCTGGGAGACACACAGGCGATCCATGCTCCATCTTCAGACACACATC 840
Db |||||
1237 AGGACAGAGCTGGGAGACACACAGGCGATCCATGCTCCATCTTCAGACACACATC 1296
QY 841 GGGCCCATCTTCTGCTGCTGTGCTCAAGAGCCCGGAGCTGGCGGCCAGCCAGACACATAC 900
Db |||||
1297 GGGCCCATCTTCTGCTGCTGTGCTCAAGAGCCCGGAGCTGGCGGCCAGCCAGACATAC 1356
QY 901 CTGGCCGTGGCGAGAACTGGCGGATGTTTCCGAAAGTACTTCGATGGAATCAACAG 960
Db |||||
1357 CTGGCCGTGGCGAGAACTGGCGGATGTTTCCGAAAGTACTTCGATGGAATCAACAG 1416
QY 961 AAGGCCCGGCGCCCGAGGCTGAGGATGAGAGGTTGGCGCGAGGCTTTGGGCTGAAAGT 1020
Db |||||
1417 AAGGCCCGGCGCCCGAGGCTGAGGATGAGAGGTTGGCGCGAGGCTTTGGGCTGAAAGT 1476
QY 1021 GCCCGCTGTGGGCTTGAAGCTCCCTCTGTGAGGAGAGCGCCCTCCCGAGATACCT 1080
Db |||||
1477 GCCCGCTGTGGGCTTGAAGCTCCCTCTGTGAGGAGAGCGCCCTCCCGAGATACCT 1536
QY 1081 CTGAGAGCAGATTGAAGCAGATGGCGCTCCAGACCGGAGGAGAGCTGTCGCCATGC 1140
Db |||||
1537 CTGAGAGCAGATTGAAGCAGATGGCGCTCCAGACCGGAGGAGAGCTGTCGCCATGC 1596
QY 1141 CGGAGCTCTTGGCAGCTACTGAGCGGGAGACCCAGGATGGCGGCGCGCA 1193
Db |||||
1597 CGGAGCTCTTGGCAGCTACTGAGCGGGAGACCCAGGATGGCGGCGCGCTA 1649

RESULT 10
AC019238/c
LOCUS Homo sapiens chromosome 19 clone RP11-700B5, WORKING DRAFT
DEFINITION Homo sapiens chromosome 19 clone RP11-700B5, WORKING DRAFT
ACCESSION AC019238
VERSION AC019238.5 GI:9838316
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Sequence Comparison

AC019238 204340 bp DNA linear HTG 17-AUG-2000
Homo sapiens chromosome 19 clone RP11-700B5, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC019238
AC019238.5 GI:9838316
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 204340)
Waterston, R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:9280808.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Center project name: H.NH0700805
----- Summary Statistics -----
Sequencing vector: M13; 84
Chemistry: Dye-terminator Big Dye; 16
Chemistry: Dye-terminator Big Dye; 16 of reads
Assembly program: Phrap; version 0.950319
Consensus quality: 199676 bases at least Q40
Consensus quality: 200928 bases at least Q30
Consensus quality: 201749 bases at least Q20
Insert size: 236000; agarose-1p

Insert size: 204523; sum-of-contigs
Quality coverage: 6.54 in Q20 bases; agarose-1p
Quality coverage: 7.57 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1
* 2752: contig of 2752 bp in length
* 2753: gap of unknown length
* 2853: contig of 3049 bp in length
* 5902: gap of unknown length
* 6002: contig of 6964 bp in length
* 12965: gap of unknown length
* 13066: contig of 7953 bp in length
* 21018: gap of unknown length
* 21119: contig of 9281 bp in length
* 30499: gap of unknown length
* 30400: contig of 10459 bp in length
* 40958: gap of unknown length
* 40959: contig of 11122 bp in length
* 52180: gap of unknown length
* 52181: contig of 12395 bp in length
* 62275: gap of unknown length
* 65276: contig of 29786 bp in length
* 95161: gap of unknown length
* 95162: contig of 27277 bp in length
* 95262: gap of unknown length
* 122638: contig of 33140 bp in length
* 122639: gap of unknown length
* 155778: contig of 48462 bp in length.
* 155779: gap of unknown length
* 155879: contig of 48462 bp in length.

FEATURES

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/db_xref="taxon:9606"
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/note="assembly_name:Contig28"

ORIGIN

Query Match 53.5% Score 966.4; DB 2; Length 204340;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:04:51 ; Search time 735 Seconds
(without alignments)
10449.989 Million cell updates/sec

Title: US-10-015-393A-115

Perfect score: 1808
Sequence: 1 gagtaccaggcggtgtggt.....actctcaaaactgtcattt 1808

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
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2	1808	100.0	1808	4	Aaf54284 DNA encod
3	1808	100.0	1808	8	ACD68321 Novel hum
4	1808	100.0	1808	8	ACH04423 Human CDN
5	1808	100.0	1808	8	ACD67967 Novel hum
6	1808	100.0	1808	8	ADCI17984 Human PRO
7	1808	100.0	1808	9	ADD70630 Human CDN
8	1808	100.0	1808	9	ADD39707 Human CDN
9	1808	100.0	1808	9	ADD70153 Human CDN
10	1808	100.0	1808	9	ADD38274 Human CDN
11	1808	100.0	1808	9	ADD39230 Human CDN
12	1808	100.0	1808	9	ADD38753 Human CDN
13	1808	100.0	1808	9	ADD40184 Human CDN
14	1808	100.0	1808	9	ADE50405 Human CDN
15	1808	100.0	1808	9	ADE20017 Human CDN
16	1808	100.0	1808	9	ADE49928 Human CDN
17	1808	100.0	1808	9	ADE21486 Human CDN
18	1799.2	99.5	2069	8	AAD56357 Human sec
19	1792	99.1	1878	5	Aaf93783 Human CDN
20	1231.4	68.1	1282	4	ADD03940 Human dru
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22	1189.8	65.8	1699	6	ABK15714 Human 216
23	1150.2	63.6	1195	6	ABK35374 Human CDN

ALIGNMENTS

RESULT 1

AAA37054
ID AAA37054 standard; cDNA; 1808 BP.
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AC AAA37054;
XX
DT 08-AUG-2000 (first entry)
XX
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DE Human PRO1430 (UN0736) cDNA sequence SEQ ID NO:115.
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KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.

XX
FN WC200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099336P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.

ALIGNMENTS

RESULT 1

AAA37054
ID AAA37054 standard; cDNA; 1808 BP.
XX
AC AAA37054;
XX
DT 08-AUG-2000 (first entry)
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XX
DE Human PRO1430 (UN0736) cDNA sequence SEQ ID NO:115.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS Homo sapiens.

XX
FN WC200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
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PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
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Sequence Comparison
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Sequence Comparison

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 PD 28-DEC-2000.
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 PF 18-FEB-2000; 2000WO-US004342.
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 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028511.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy WA, Smith V, Stewart TA, Tamas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2001-071395/08.